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us-09-026-459a-28

January 16, 2003, 15:20:22 : Search time 70.8983 Seconds
(without alignments)
14944,909 Million cell updates/sec

Perfect score: 3455

Sequences: 1 GCGCTGATGACAGACAGAGG.....AAATGAGGATTAATGATAGT 3455

Scoring table: IDENTITY NUC

Gapop 10.0 : Gapext 1.0

Searches: 44162 seqs, 15558381 residues

Total number of hits satisfying chosen parameters: 88274

Minimum DB Seq length: 0

Maximum DB Seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cmap2/6/ptdata/1/ina/5A_COMB.seq.*
- 2: /cmap2/6/ptdata/1/ina/6A_COMB.seq.*
- 3: /cmap2/6/ptdata/1/ina/6A_COMB.seq.*
- 4: /cmap2/6/ptdata/1/ina/6B_COMB.seq.*
- 5: /cmap2/6/ptdata/1/ina/6B_COMB.seq.*
- 6: /cmap2/6/ptdata/1/ina/7A_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4222.4	94.3	4232	1	US-08-048-760-1
2	4222.4	94.3	4232	1	US-08-048-760-2
3	4222.4	94.3	4232	2	US-08-470-091-1
4	4222.4	94.3	4232	2	US-08-470-091-2
5	2755.6	79.7	2994	1	US-08-204-429-2
6	2755.6	79.7	2994	2	US-08-482-027-4
7	2755.6	79.7	2994	4	US-08-801-092-4
8	2755.6	79.7	2994	4	US-08-315-113-4
9	2755.6	79.7	2994	5	PER US94-10457-1
10	2755.6	79.7	2994	5	US-08-956-648-7
11	2755.6	79.6	2993	4	US-08-428-674A-7
12	68.8	2.0	2808	1	US-07-708-962-1
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14	68.2	2.0	3249	1	US-08-429-264-1
15	68.2	2.0	4853	1	US-08-842-883-1
16	68.2	2.0	4853	4	US-08-842-877-1
17	65.6	1.9	2408	2	US-08-152-2218-1
18	59	1.7	7218	1	US-08-242-463-14
19	51	1.5	4747	4	US-09-213-2940-2
20	44.6	1.3	1803	4	US-09-144-001C-799
21	44.6	1.3	15463	4	US-08-961-527-139
22	44.4	1.3	20674	4	US-09-641-638-651
23	44	1.3	19124	2	US-08-487-826B-13
24	43.8	1.3	1056	4	US-09-144-001C-1550
25	43.2	1.3	509	4	US-09-979-007-202
26	43.2	1.3	509	4	US-09-605-785-202
27	43.2	1.3	509	4	US-09-446-413-202

28	43.2	1.3	509	4	US-09-452-616A-202
29	43.2	1.3	509	4	US-09-242-149A-202
30	43	1.2	5852	1	US-07-867-106-2
31	42.8	1.2	615	4	US-08-998-416-186
32	42.6	1.2	1189	1	US-08-307-591-2
33	42.6	1.2	2604	4	US-09-244-827B-4
34	42.4	1.2	1186	2	US-08-741-722-5
35	42	1.2	665	2	US-08-883-755A-46
36	42	1.2	1864	4	US-09-468-265-4
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38	41.4	1.2	19124	2	US-08-487-826B-13
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41	41.2	1.2	2030	2	US-08-785-937-7
42	40.6	1.2	860	4	US-08-998-416-287
43	40.6	1.2	4078	2	US-08-960-022-3
44	40.6	1.2	6265	4	US-09-129-112-3
45	40.6	1.2	12124	1	US-08-161-271A-56

ALIGNMENTS

RESULT 1
US-08-038-760-1
Sequence 1, Application US/08048760
Patent No. 5496741
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Bu, Shi-Xue
TITLE OF INVENTION: B: of Specific Lab. 2-Effect of Genes on Gene Products and
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: pc DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/048,760
FILING DATE: 19940325
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19..2469
US-08-038-760-1

Query Match: 94.3%, Score 4222.4, DB 1, Length 4232
Best Local Similarity: 100.0%, Freq. 101.01
Matched 3232, Conservative 0, Mismatches 1, Gaps 0

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1730 CTTCTAACATCTTAAATAAAGGTTTCAACCTACCGGCTTAATCTTACATCTTAAATCTA 1671
1792 GAGACAAAGCAAGCTCAGGCTTCCAGACGACGAGAGGACATCAAAATCTATCTCTCTTCA 1851
1670 GAGACAAAGCAAGCTTCCAGACGACGAGAGGACATCAAAATCTATCTCTCTTCA 1611
1852 CTGTTTTATAAANAATGATGAGGCTAGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1621
1610 CTGTTTTATAAANAATGATGAGGCTAGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1551
1912 CTGCT 1971
1550 CT 1491
1972 GAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2031
1490 GAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1431
2032 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2091
1430 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1371
2092 AAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2151
1370 AAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1311
2152 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2211
1310 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1251
2212 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2271
1250 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1191
2272 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2331
1190 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1131
2332 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2391
1130 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1071
2392 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2451
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2452 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2511
1010 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
2512 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2571
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892 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
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1132 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1191
2330 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2271
1192 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2211
2270 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2151
2212 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2091
2152 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2031
2090 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1971
2032 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
1972 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1851
1910 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1791
1852 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1731
1790 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1671

[illegible]

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Db      2760 ACTAGCTTTTGATATTGAAAGATAGATGAATAGATGGAAATGAACATGTCCAGAGA 2811
QY      2589 GUCCAATTTTCACGACAAAACGCCAGAAAACGACATTCACGCGAACACGAAATGCAGAAAGTA 2648
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Db      2820 GUCCAATTTTCACGACAAAATGCCAGAAAATCAGTTCACGCGAACACGAAATGCAGAAAGTA 2879
QY      2649 GAATAATCATATATATATATATATATATATATATATATATATATATATATATATATATAT 2708
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Db      2880 CAAATTCAGATGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2939
QY      2709 TTTTTCATATATTCATATATATATATATATATATATATATATATATATATATATATATATATAT 2763
Db      2940 TATGACATATATGATATATATATATATATATATATATATATATATATATATATATATAT 2994

RESULT 6
US-08-482-627-4
: Sequence 4, Application US/08482627
: Patent No. 5998134
: GENERAL INFORMATION:
:   APPLICANT: Icc, Wen-Hwa
:   TITLE OF INVENTION: Refinoblastoma Gene Cancer Suppressor
:   NUMBER OF SEQUENCES: 5
:   NUMBER OF SEQUENCES: 5
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Campbell and Flores
:     STREET: 4370 La Jolla Village Drive, Suite 700
:     CITY: San Diego
:     STATE: California
:     COUNTRY: United States
:     ZIP: 92122
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patent In Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/482,627
:     FILING DATE: 07-JUN-1995
:     CLASSIFICATION: 435
:   PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: US 07/951,947
:     FILING DATE: 28-SEP-1992
: ATTORNEY/AGENT INFORMATION:
:   NAME: Campbell, Cathryn A.
:   REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-UC 1707
TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 4:
: SHORCE CHARACTERISTICS:
: LENGTH: 2994 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
:   NAME/KEY: CDS
:   LOCATION: 139..2924
: US-08-482-627-4

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3

COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,883
FILING DATE:
CLASSIFICATION: 445
ATTORNEY/AGENT INFORMATION:
NAME: Medaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/WORKET NUMBER: 8321-13 US1
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4853 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
POLYMER: linear
MODIFIED TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 70..3489
US-08 832,883-1

Query March 2, 2003; Score 68.2; DB 1; Length 4853;
Best Local Similarity 53.0%; Prod. No. 1.4e-06;
Matches 170; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QV 1823 ASAAAGGATTCGAAATGACCTCTTTCAGCTGTTTATAAAAAGTGTATCGCTAGCT 1882
DB 2552 ATAGATGAGGAGACGACCTCTTTCAGCTGTTTATAAAAAGTGTATCGCTAGCT 2611
QV 1883 ATCTCGGATTAATATATATTTTGTGAAAGCTTCTGCTGAGGACCGGAAATTAAGACATA 1942
DB 2412 CTGTGACCTTGGGATCTGTATGATGATATATTTTATATATTTTATATATTTTATATAT 2668
QV 1943 TCAATCTGACCTTCTTCTGACGACCTTCTGACGACCTTCTGACGACCTTCTGACGACCT 2002
DB 2669 AAATCTGACCTTCTTCTGACGACCTTCTGACGACCTTCTGACGACCTTCTGACGACCT 2728
QV 2003 ATTTGACGACCTTCTTCTGACGACCTTCTGACGACCTTCTGACGACCTTCTGACGACCT 2062
DB 2729 ATCTGACCTTCTTCTGACGACCTTCTGACGACCTTCTGACGACCTTCTGACGACCTTCT 2788
QV 2063 TTAATTTGAAATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2122
DB 2789 AGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2848
QV 2123 TCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2183
DB 2849 ATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2869

Search completed: January 17, 2003, 18:19:19
Job time: 107.898 secs

QY 242 AspHisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 261
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DB 1160 GATCAIATAAAGTCTTCAGTGTGATTCATAGACAGATTTTGAACACACAGAACACCA 1209
QY 262 ArgLysSerAsnLeuAspGlnIleValAsnValIleProProHisThrProValArgThr 281
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DB 1210 CGAAAAAGTAAAGCTTCAGCAACACCGCAAGTAAATTCCTCCACACACACACACCAAGT 1269
QY 282 ValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 301
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DB 1270 GTATAGAAACTATGCAACAACTTAATGATGATTTTAAATTCAGCAAGGATCAACCTTCA 1329
QY 322 GluAsnLeuIleSerThrPheAsnAsnCysThrValAsnProGlySerIleLeuLys 321
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DB 1400 GAAATTCATTTCCATTTTAAACAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1389
QY 342 ArgValLysAspIleGlyThrIlePheLysGlnLysPheAlaLysAlaValGlyGlnGly 341
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DB 1490 AGATTCAGGATATAGCATACATCTTTAAAGACAAATTTGCTTAAAGCTGTGGCAGAGGT 1449
QY 362 CysValMetIleLeuSerGlnArgThrLysLeuGlyValArgLeuThrArgValMet 361
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DB 1490 TGTGTGCAATTCATCAGCAAGCAATCAAACTTGGAGTTGGTTGATTAAGCAAG 1509
QY 382 GluSerMetLeuLysSerGluGlnArgLeuSerIleGlnAsnPheSerLysLeuLeu 381
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DB 1510 GAATCAATGCTTAAATTCAGAAAGCAAGATATATCATCAAAATTTTAAAGCAATTCGTG 1569
QY 402 AsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGlnValValMetAlaThr 401
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DB 1570 AATCAACAATTTTCATATGCTTTATTCGGCTGCGCTTCCTTCAGGTGTGAAGGCCACA 1629
QY 422 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProThrIle 421
|||||
DB 1600 CTGAATGCTTAAATTTAAAGCTTTGATTTTAAAGTATGATGAAAGTTTATCAAA 1749
QY 442 AlaGlnGlyAsnLeuThrArgGlnMetIleLysHisLeuGlnArgCysGlnHisArgIle 461
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DB 1750 GATCAAGCAATCAATTCAGCAAAATCAAAATTTAGAACGATGCAACATCGAATC 1809
QY 462 MetGlnSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLys 481
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DB 1810 ATGAAATTCCTTCATGAGCTCTCAATTCATTCATTTATTTATTTATTTAAATTAAG 1869
QY 482 AspArgGlnGlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeuProLeuGln 501
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DB 1870 GAGGCAAAAGCAAT 1929
QY 502 AsnAsnHisThrAlaAlaAspMetThrLeuSerProValArgSerProLysLysGly 521
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DB 1940 AATAATCACACGCCAGCATATGATCTTCCTCGTGAAGATCTCCAAAGAAAAAGCT 1989
QY 522 SerThrThrArgValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAlaPheGln 541
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DB 1990 TCAATATAGAGTGAATATCTATATGAAAGAGAGACAAAGCAAGCTCAGCTTCAG 2049
QY 542 ThrGlnLysProLeuLysSerThrSerLeuSerLeuPheThrLysLysValThrArgLeu 561
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DB 2050 AAGCAAAAGCAATTCAGATTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2109
QY 562 AlaTyrLeuArgLeuAsnThrLeuLysGlnArgLeuLeuSerGlnHisProLeuGln 581
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DB 2110 GATATATCGCGGTAATAATATCTTCTCAACCGCTTCCTCGCAGCAGCCCAAGATTAGAA 2169
QY 582 HisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlnThrGlnLeuMetArgAsp 601
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DB 2170 CATATATATGAGACCTTTTTCAGTACACCGCTGAGCAATGATGATGATGATGATGATG 2229
QY 602 ArgHisLeuAspGlnIleMetPheThrLysSerMetThrLysLysValLysAsnIle 621

DB 2230 ACCCATTTGACCAAAATATATGATGATGATGATGATGATGATGATGATGATGATGATG 2289
QY 622 AspLeuLysPheLysIleValThrAlaTyrLysAspLeuProHisAlaValGlnGly 641
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DB 2290 GAGCTTAAATTTAAATTCATCTTAAACAGCATACAAAGATTCCTCCACACACACCAAG 2349
QY 642 ThrPheLysArgValLysIleLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 661
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DB 2350 AATTCAGAGGTTTGTGATCAAAAGAGAGAGATGATGATGATGATGATGATGATGATGAT 2409
QY 662 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnGlnGlnGlnGlnGlnGln 681
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DB 2410 TCGGTCTTCATGACAGACATGAAAAACAATAATTTCCAGTATGCTTCACCAAGCGCTT 2469
QY 682 ThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 761
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DB 2470 AACTTCACCAAAATCACTCACTTCGAAAGCGCTTCAAGTTTCCTAGTTCAAGCTTCA 2529
QY 702 ArgIleProGlyGlyAsnIleCysThrIleSerProLysSerProGlyThrLysIleSerGln 721
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DB 2530 CGCATTCCTGAGAGCAATATATATTTTACCGCTGAAAGTCAATATAAATTTTCAAA 2589
QY 722 GlyLeuProThrProGlnLysMetThrPheArgSerArgIleLeuValSerIleGlyGln 741
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DB 2590 GGTCTGCCAACACCAACAAAAATGATCCAGATCAAGAAATCTTAAATATCAATTCGCAAA 2649
QY 742 SerPheGlyThrSerGlnLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 761
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DB 2650 TCATTCGGAGCTTCGAGAGTTCCAGAAAAATAATTCATGCTATGTAACAGCGACGGT 2709
QY 762 ValLeuLysArgSerAlaGlnGlySerAspThrProGlyLysProLeuLysLeuArgPhe 781
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DB 2710 GTATTCAAAAAGATTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2769
QY 782 AspIleGlnGlySerAspGlnAlaAspGlySerLysHisLeuProGlyCysLysPhe 801
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DB 2770 GATATTCAGCATCATCATCAACACATGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2829
QY 802 GlnGlnLysLeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsn 821
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DB 2830 CAGCAACAAATCCGACAAATGATCTTCTTCCACACCAAGATCCAAAGCAAAATCAAT 2889
QY 822 AspSerMetAspThrSerAsnLysGluGlnLys 832
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DB 2890 GATAGCATGATATACCTTAAATTAAGCAAAAGCAAA 2922

RESULT 3

US-08-801-092-3

; Sequence 3, Application US/08801092

; Patent No. 6074850

; GENERAL INFORMATION:

; APPLICANT: Autelmann, Douglas

; APPLICANT: Gregory, Richard J.

; APPLICANT: Walls, Kenneth N.

; TITLE OF INVENTION: Tissue Specific Expression of

; TITLE OF INVENTION: Receptor-Like Protein

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: CA USA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/801,092

; FILING DATE: 14-FEB-1997


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QY 412 ValLeuSerArgSerThrSordInAsnLeuAspSerGlyThrAspLeuSerPheProIrrPile 421
DB 410 IATAAGAAAGTACATCTGAAATCTTGATCTGGACAGATTGTCTTCCCATGGATT 1689
QY 412 LeuAsnValLeuAsnLeuLysAlaPheAspPheTyrlLysValIleGluSerPheIleLys 441
DB 410 CTGAAAGTGGTAAATTAAGAGCTTGGATTTTACAAAGTTCATCGAAAGTTTACAAA 1749
QY 412 AlaGluAlaGluLeuThrArgGluMetIleLysHisLeuGluArgCysGluIleSerIle 461
DB 410 GTACAGAGCAACTTGGACACAGCAATATCAATAACATTTAGAACGATGTCAACATCGAATC 1809
QY 412 MetGluSerLeuAlaThrLeuLeuSerProLeuPheAspLeuIleLysGlnSerLys 481
DB 410 ATGAAATCGCTGTATGATGAGTCTGATGATTCAGATTCAGTTTATTTGATCTTATTAACAAATCAAG 1869
QY 412 AspArgAlaGluProThrAspPheIleGluSerAlaCysProLeuAsnLeuProLeuGln 501
DB 410 GACGACAGAGGATCACTGATCACTGATCACTGATCACTGATCACTGATCACTGATCACTGATCACT 1929
QY 512 AsnAsnHisThrAlaAlaLysPheLeuLeuSerProValArgSerProLysLysLys 521
DB 510 AATAACACACTGGACACATATGATATCTTCCCTGTAAGATCTCCCAAGCAAAAAGGT 1989
QY 512 SerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGln 541
DB 510 TCAACTAGCGGTATAATTCTATTAATATGAGAGAAATGAAATGATATGAAATGATATGAAATG 2049
QY 512 ThrGluLysProLeuLysSerThrSerLeuSerLeuPheLysValTyArgLeu 561
DB 510 ACCGACAGAGGATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2109
QY 512 AlaTyrlLeuArgLeuAsnThrLeuGluGluArgLeuLeuSerGluHisProGlnLeuGln 581
DB 510 GCCATCTCCGGCTAAATATACATCTTGGACCGCTCTCTGACAGCCACCACCAATTAAG 2169
QY 512 HistIleIleThrPheLeuPheGluHisIleIleGluHisIleGluHisIleGluHisIle 601
DB 510 CATATCATCTGAGAGCTTTTCTGACAGAGCTGCTGCAATGATGATGATGATGATGATGATGATG 2229
QY 512 ArgHisLeuAspGlnIleMetMetCysSerMetThrGlyLeuGlySerValLysAsnLeu 621
DB 510 ACATATCTGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2289
QY 612 AspLeuLysPheLysIleIleValThrAlaTyrlLysAspLeuProHisAlaValIleGln 641
DB 610 GACCTTAAATTCAGAAATCATCTGAAAGATATCAAGGATCTCTCCCACTCTCTCTCTCTCTCTCT 2349
QY 612 ThrPheLysArgValLeuIleIleLysGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 661
DB 610 AATTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2409
QY 612 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnIleTyrlAsSerThrArgProPro 681
DB 610 TCCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2469
QY 612 ThrLeuSerProIleProHisIlePheArgSerProTyrlLysPheProSerProLeu 701
DB 610 AATCTGACAGCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2529
QY 702 ArgIleProLysGlyAsnLeuThrLeuSerProLeuLysSerProTyrlLysSerGln 721
DB 700 GATATCTGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2589
QY 712 ArgPhePheThrProThrLysMetThrProArgSerArgIleGluValGluIleGluGln 741
DB 710 GATCTGACCAATACCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 2649
QY 712 SerPheLysThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 761
DB 710 TCACTGAGCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2709

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QY 762 ValLeuSerArgSerAlaLeuGlySerAsnProLeuGlnSerPheProIrrPile 781
DB 710 GTGCTAAAGAAATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2769
QY 782 AspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 801
DB 710 GATATGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2829
QY 802 GlnGluLysLeuAlaGluMetThrSerThrArgThrArgMetGlnGlySerLysMetAsn 821
DB 810 CAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2889
QY 822 AspSerMetAspThrSerAsnLysGlnGluLys 842
DB 810 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2922

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RESULT 8

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US-08-038-760-1
: Sequence 1, Application US/08038760
: Patent No. 5496731

```

GENERAL INFORMATION:

```

: APPLICANT: Xx, Hong-Ji
: APPLICANT: Hu, Shi-Xue
: APPLICANT: Benedict, William F.
: TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
: TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711

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COMPUTER READABLE FORM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/038,760
: FILING DATE: 19930125
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 7409-025-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE

```

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

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: LENGTH: 3232 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 19..2469
US 08 038-760-1

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Alignment Scores:

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Pred. No.: 0 Length: 3232
Score: 4213.00 Matches: 820
Percent Similarity: 100.00% Conservative: 0
Host Local Similarity: 100.00% Mismatches: 0
Query Match: 98.48% Indels: 0
DB: 1 Gaps: 0

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US-09-026-459a-35 (1-832) x US-08-038-760-1 (1-3232)

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QY	13	AspGluAspGlnMetSerPheThrPheThrGluLeuGlnLysAsnIleGglllleSerVal	32
ID	17	GGCTAGATGAGATGCGTTCACCTTTTACAGGTACAGAAAAACATAGAAATCATGTGC	66
QY	33	HistLysPhePheAsnLeuLeuLysGlnIleAspThrSerThrLysValAspAsnAlaMet	52
ID	67	CATAAATCCTTAATTAATAAAACAATGCATCCCACTACCAAGCTTGAAATGCCATAG	126
QY	53	SerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGlnArgThr	72
ID	127	TCAAAGACTTTCGAAGAATTATGATGATGTTTCATCTCTTCAGCAAAATTCGAAGAGCA	186
QY	73	CysThrLeuLeuLeuThrLeuThrProSerSerIleSerThrGluIleAsnSerAla	92
ID	187	TGTGAATTAATAATTAAGAACAGAGTTCGATATGCTATGAAATAAATTCGTCA	246
QY	93	LeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGlyValLeuGlnMet	112
ID	247	FCTGGCTAAAAGCTTCCTGGACACATTTTTATAGCTAAAGGGCAAGTATACAAATG	306
QY	113	GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLys	132
ID	307	GAAAGATGATCTGCTGATATTCATTCAGTAAAGTATGTTGCTTGAATATATATAAA	366
QY	133	LeuSerProHemMetLeuLeuLysGlnProLysThrAlaValIleProIleAsnGly	152
ID	367	CTCTACCTCCCATCTGCTCAAAACACATATAAACAGTGTGTATACCATTAATGGT	426
QY	153	SerProArgThrProArgArgGlyHisAsnArgSerAlaArgIleAlaLysGlnLeuGln	172
ID	427	TCACTTCGAACACCACCGACGTCAGAGCACAGACGACGTACCGATACCAACCACTAGAA	486
QY	173	AsnAspThrArnlleIleGluValLeuCysLysGlnIleHisGluCysAsnIleAspGluVal	192
ID	487	AATGAINCANGAATTATTGNAAGTCTCTGTGTAANAANATGAATCTAATATATAGAGGTG	546
QY	193	LysAsnValTyrPheLysAsnPheIleProHemMetAsnSerLeuGlyLeuValThrSer	212
ID	547	MAAATGTTTATTCAAAAATTTATACCTTTTAGTAATCTCTTGCAGCTGTAAACATCT	606
QY	213	AsnGlyLeuProGlnValGluAsnLeuSerLysArgTrpGluGluIleTyrLeuLysAsn	232
ID	607	AATGCACTTCACAGGTTCAAAACCTTCTCAACGATACGAAGAAATTAATCTTAAAAAT	666
QY	233	LysAspLeuAspAlaArgIlePheLeuAspHisAspLysThrLeuGlnTyrAspSerIle	252
ID	667	AAGAATCATGATCAAGATATATTTTGGATCATGATATAAATCTTCAACATGATTCTATA	726
QY	253	AspSerPheGlnThrGlnArgThrProArgLysSerAsnLeuAspGluGlnValAsnVal	272
ID	727	GACAGTTTGGAAATCAAGAAATCAAGAAAAAGTAACTTGAIGAAGAGAGGTGAATGTA	786
QY	273	IleProProGlnThrPheValArgThrValMetAsnThrIleGlnIleLeuMetMetIle	292
ID	787	ATTCTCCATCACATCCAGCTAGACACTGCTAAGACACTATCCAACAAATTAATCAATGATT	846
QY	293	LeuAsnSerAlaSerAspGlnProSerGlnAsnLeuIleSerTyrPheAsnAsnCysThr	312
ID	847	TTAAATTCAGCAAGTGATCAAGCTTCAGAAAATGTGATTCTCTATTTTAACTATGACCA	906
QY	313	ValAsnProLysLysSerGlnLeuLysArgValValLysAspIleGlyTyrIlePheLysGlu	332
ID	907	GTCAAATCAAAAACAAAGTATATCTGAAAACATGGAAGATATAGATATCATCTTTTAAAGAG	966
QY	333	LysPheAlaLysAlaValGlyGlnGlyCysValGlnIleGlySerGlnArgTyrLysLeu	352
ID	967	AAATTCGCTAAAATGCTGGAAATAGCGTCTGCTGAAAATTCATATCACACCAACAACTT	1026
QY	353	GlyValArgLeuTyrTyrArgValMetGlnSerMetLeuLysSerGlnGlnArgLeu	372
ID	1027	GGAGTTCGGTGTATATAGAGATAAGGAATTCATATGCTTAAATCAGAAGAGAAAGATTAT	1086
QY	373	SerIleGluAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAla	392

Db	1087	JCCATTTCAAAATTTAGTAAAGTCTGGAAACAAATATTTCTATATCTTTATATCGCG	1147
QY	393	CysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGluAsnLeuAspSer	412
Db	1147	TGGGCTCTTCAAGTCTGTAAGGCCACATAAGTACAAATACATTCAGAAATTCATATCT	1206
QY	413	GlyThrAspLeuSerProHoriTrpIleLeuAsnValIleuAsnIleuLysArgAspGlu	432
Db	1207	GGAAACAGATTCTCTTCTCATGGATCTCGAATGTCTTAATTTAATAAAGCTTTGATTTT	1266
QY	433	TyrlsValIleLeuSerPheIleLysAlaIleuLysAsnLeuThrArgLeuMetIleLys	452
Db	1267	TACAAAGTCATCGAAAGTTTATCAAGGTACAAAGGTAACTGCATACAAATTCATAAAA	1326
QY	453	HisLeuGluArgCysGluHisArgIleMetIleLysLeuAlaIleLysLeuSerAspSerPro	472
Db	1327	CAATTACAAACGATGTCGAATACGAAATCAAGAAATCTTCCATACGCTTCATATCAATCT	1386
QY	473	LeuPheAspLeuIleLysIleSerLysAspArgIleuLysProThrAspHisLeuLeuSer	492
Db	1487	TTATTTTCATCTATTATAAATCAAGAGACGTGAAAGAGTAACTGATCTACTTGAAATCT	1446
QY	493	AlaCysIleProLeuAsnLeuProLeuGluAsnAspHisThrAlaIleAspMetTyrLeuSer	512
Db	1447	GCCTGCTCTTAATCTCCCTCCAGAAATACACACAGCTGACATGATATCTCTCTCT	1506
QY	513	ProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla	532
Db	1507	CCCTCTAAGATCTCCAAAGAAAAAGGCTCAATACCGCGTCTAAATTCATCTCAATCTGA	1566
QY	533	GluThrGluAlaThrSerAlaPheGluThrGluLysProLeuLysSerThrSerLeuSer	552
Db	1567	GAAATCAACAGTAATCTACGCTCTTCAGATCAATCAAAATATGAAATTAATCTTTCTA	1626
QY	553	LeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuLysLeuArg	572
Db	1627	CTGTTTATAAAAAAGCTGATCGGCTAGCGTACGCTACCGGCTAAAATACATCTTGCAATGC	1686
QY	573	LeuLeuSerGluHisProIleuLeuHisIleIleTyrThrLeuPheLeuHisThrLeu	592
Db	1687	CTTCTGCTGAGGACCCCAATATGAACATATCATCTGCAGATTTTCTATCATATCTG	1746
QY	593	GluAsnGluTyrGluLeuMetArgAspArgHisLeuAspGluIleMetMetCysSerMet	612
Db	1747	CAGAAATGATATGAACTCATGATAGACAGCATTTGATCAATAATATCATGTGTTTCATG	1806
QY	613	TyrCysIleLysValLysAsnIleAspLysLysPheLysIleLeuValAlaTyr	632
Db	1807	TATGGCATATGCCAAGTGAAGATATAGACCTTAATATCAAAATCATCTGTAACATATAC	1866
QY	633	LysAsnLeuProHisAlaValGluGluThrPheLysArgValLeuIleLysLeuLeuLeu	652
Db	1867	AAGATCTTCCATCATCTCTCAGACAGACATCAAAAGCTTTTCATCAACACATACAG	1926
QY	653	TyrAspSerIleIleValPheTyrAsnSerValPheMetGluArgLeuLysThrAsnIle	672
Db	1927	TATGATCTATTATAGTATCTATATACTCGCTGCTCATGACAGATACGAAAAAATAAT	1986
QY	673	LeuGluTyrAlaSerThrArgProThrLeuSerProIleProHisIleProArgSer	692
Db	1987	TTGCAGATGCTTCCACCAAGGCGGCTAGCTGTCATCAATCAATCAATCTCTCAAGCT	2046
QY	693	ProTyrLysPheProSerSerProLeuArgIleProLysLysAsnIleTyrIleLeuPro	712
Db	2047	CCCTACAAAGTTCCTAGTTCATCCCTTACGGATTCGGAAGCAAAATATATATATCAATCT	2106
QY	713	LeuLysSerProTyrLysIleSerGluLysLeuProThrProThrLysMetThrProArg	732
Db	2107	CTGAAGATGCTATATAAATTTTCAAGGCTCTGGTAACTCAATCAATCTCTCAAGCT	2166
QY	733	SerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheLeuLysIle	752

21 2107 PAAAGAAATTGATATCAATTGGTGAATCATTGCGGACCTTCTGAGAAAGTTCCAGAGAAATA 2226
 QY 753 ASNGINMETVALCYASASerAspArgValHeuLysArgSerAlaGluGlySerAsnPro 772
 DB 2227 AALCAGAGGTAAGAAAGAGGATGCGTGTGCTGCAAAAGAGCTGCTGAAGGAGGCAAGCCCT 2286
 QY 772 PPTGSEPTLEUPLYSSTETCAAPheAspTleGluGlySerAspGluAlaAspGlySer 792
 DB 2287 ACIAAAACACIAAAACACIACGCTTCATATCGAAGGATTCAGATGAAGGAGAGATGGCAAGT 2346
 QY 792 TSHSISLSTPSTGlyGlySerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArg 812
 DB 2347 AAGCATCTGGCAGGAGAGATGCAATATTCAGCAAGAAATGAGAAATGAGATGATTTATTTGA 2406
 QY 812 ThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 832
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RESULT 4

US-08-038-760-2/2
 1 Sequence 27, Application US/08038760
 2 Patent No. 6496741
 3 GENERAL INFORMATION:
 4 APPLICANT: Xu, Hong-Ji
 5 ATTORNEY: Hui, Shi-Xue
 6 TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and
 7 METHOD OF INVENTION: Methods for Tumor Suppressor Gene Therapy
 8 NUMBER OF SEQUENCES: 3
 9 RESPONDENT'S ADDRESS:
 10 ADDRESSEE: Pennie & Edmunds
 11 STREET: 1155 Avenue of the Americas
 12 CITY: New York
 13 STATE: New York
 14 COUNTRY: U.S.A.
 15 ZIP: 10036-2711

16 MODER REABLE FORM:
 17 MEDIUM TYPE: Floppy disk
 18 COMPUTER: IBM PC compatible
 19 OPERATING SYSTEM: DOS/Windows
 20 SOFTWARE: Patent Release #1.0, Version #1.25
 21 CURRENT APPLICATION DATA:
 22 APPLICATION NUMBER: US/08/038,760
 23 FILING DATE: 1998/03/26
 24 CLASSIFICATION: 424
 25 ATTORNEY/AGENT INFORMATION:
 26 NAME: Polissant, Brian M
 27 RESIDENCE NUMBER: 28 443
 28 REFERENCE NUMBER: 29 7406-026-009
 30 TELECOMMUNICATION INFORMATION:
 31 TELEPHONE: (212) 790-9090
 32 TELEFAX: (212) 829-9741/8264
 33 INDEX: 56141 PENNIE
 34 INFORMATION FOR SEQ ID NO. 2:
 35 SEQUENCE CHARACTERISTICS:
 36 LENGTH: 242 base pairs
 37 TYPE: NUCLEIC ACID
 38 STRANDEDNESS: double
 39 ORIENTATION: not relevant
 40 MOLECULE TYPE: DNA

US-08-038-760-2

Alignment Scores:
 1 Prod. No.: 0 Length: 3232
 2 Score: 4213.00 Matches: 820
 3 Percent Similarity: 100.00% Conserved: 0
 4 Best Local Similarity: 100.00% Mismatches: 0
 5 Query Match: 98.4% Indels: 0
 6 Gaps: 0

US-09-026-459a-35 (1-832) x US-08-038-760-2 (1-3232)

1* AspLeuAspGluMetSerPheThrGluLeuGlnLysAsnGluLeuSerVal 32

DB 3230 GACCTAGATGACATGCTGCTCATTCTAGGCTACAGAAAAACATAGAAATTAAGTGC 3171
 QY 313 HistLysPheThrAsnLeuLeuLysGluGlyAspThrSerThrLysValAspAsnAlaMet 52
 DB 3170 CATAAATCTTTAACTTAATAAAAGAAATGATACCAAGTACCAAAAGTTGATAATGCTATG 3111
 QY 53 SerArgLeuLeuLysLysTyAspValLeuPheAlaLeuPheSerLysLeuLysValThr 72
 DB 3110 TCAACACACTTTCAGAGAGATATCATGTTGTTCCACATCTCAGCAAAATTCGAAAGGACA 3051
 QY 73 CysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 92
 DB 3050 TCTTAAGCTTATATATTTGACACAAAGCAAGTCTGATATCTACTGAAATATATATTCGCA 2991
 QY 93 LeuValLeuLysValSerTyrTyrPheThrPheLeuLeuAlaLysGlyGluValLeuGluMet 112
 DB 2990 TTGCTGCTAAGAAATTTTGTGATACATTTTATTAATTAAGGAGGATATACAAATG 2941
 QY 113 GluAspAspLeuValLysSerPheGlnLeuMetLeuLysValLeuAspTyrPheLeuLys 132
 DB 2930 CAAGATGATCTGCTGATTCATTTCATTAATGCTATCTGCTCCTTCACTATTAATAAA 2871
 QY 133 LeuSerProProMetLeuLeuLeuLysGluProTyrLysThrAlaValLysPheLeuAsnGly 152
 DB 2870 CTCTAT 2811
 QY 153 SerProAspGlyProArgArgGlyGlyAspArgSerAlaArgLysGluLeuLeuLeuLeu 172
 DB 2810 TAT 2751
 QY 173 AsnAspThrArgGluLeuGluValLeuLysGlyLysGluLysGluLysGluVal 192
 DB 2750 AATGATACCAAGATTTATGGAAGTCTCTGTAAGCAACATCAATTAATATATATATATAT 2691
 QY 193 LysAsnValTyrPheLysAsnPheLeuLeuProPheMetAsnSerLeuLysLeuValThrSer 212
 DB 2690 AAAAAATGTTTATTTCAAAATTTTATATATATATATATATATATATATATATATATAT 2631
 QY 213 AsnGlyLeuProGluValGlyGlyAsnLeuSerLysArgTyrGluGluLeuLeuLeuLysAsn 232
 DB 2630 ATATGACTTTCAGAGGTTGAAAATTTTCTTAAAGSATAAGSANAATTAATTAATTAAT 2571
 QY 233 LysAspLeuAspAlaArgLeuPheLeuAspLysAspLysThrLeuGlnThrAspSerIle 252
 DB 2570 AAACATCTACATGCAACATTAATTTTCTATATATATATATATATATATATATATATAT 2511
 QY 253 AspSerPheGluThrGluArgThrProArgLysSerAsnLeuAspGluGluValAsnVal 272
 DB 2510 GACACTTTTGGAAACACAGAGAACACACACACACACACACACACACACACACACACAC 2451
 QY 273 TCTPCT 242
 DB 2450 ATTAT 2491
 QY 243 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuLeuSerTyrPheAsnAsnGlyThr 312
 DB 2390 TTAAATTCAGCAAGTATCAACCTTCAGAAAATGCTATTCCTATTTTAAACACTTCACA 2131
 QY 313 ValAsnProLysGluSerIleLeuLysArgValLysAspLeuGlyTyrPhePheLeuGlu 332
 DB 2130 GTGAATCAAAAGGAAATATATCTTAAAGAGTAAAGAAATAGAAATATATATATATAT 2071
 QY 333 LysPheAlaLysAlaValGlyGlnGlyCysValGluLeuLysSerGluArgTyrLysSer 352
 DB 2070 AAAATTCATAAATTCATGAGAAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2011
 QY 353 GlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeu 372
 DB 2010 GGAATTCCT 2151
 QY 373 SerIleGlnAsnPheSerLysLeuLeuAspAsnIlePheHisMetSerLeuLeuAla 392


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Query Match: 17.9% Indels: 340
            1 Gaps: 40
135 09 026 459a 35 (1 842) x 03 07 708 962-1 (1 2808)
QY 55 LeuLeuLysLysTyAspValLeuPheAla --- LeuPheSer --- 67
DB 55 LeuLeuLysLysTyAspValLeuPheAla --- LeuPheSer --- 67
140 4 ATATTCATAAATAAAGAGAAATTTTATATATATATTTTAAATGATATGAAAGCA 63
QY 68 CysLeuAlaArgThrCysGluLeuLeuThrLeuProSerSerSerLeuSer 86
DB 68 CysLeuAlaArgThrCysGluLeuLeuThrLeuProSerSerSerLeuSer 86
145 64 CAAGATTACACA --- AGGAGGAGGAGGAGGAGGATTCCT 102
QY 80 ThrGluLeuAsnSerAlaLeuValLeuLysValSerThrPheLeuLeuAlaLys 106
DB 80 ThrGluLeuAsnSerAlaLeuValLeuLysValSerThrPheLeuLeuAlaLys 106
146 104 ATATGATTAAGAT --- GCGTTTAAATTCGTTGGACACATTTTGTGTAATAAG 156
QY 107 GlyThrValLeuGluLeuMetGluAspLeuValLeuSerPheGluLeuMetLeuCysVal 126
DB 107 GlyThrValLeuGluLeuMetGluAspLeuValLeuSerPheGluLeuMetLeuCysVal 126
147 157 GGTAAATTTGAGATGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAG 216
QY 157 GGTAAATTTGAGATGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAG 216
DB 157 GGTAAATTTGAGATGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAG 216
148 127 LeuAspTyPheLeuLys --- LeuSerPro 135
QY 127 LeuAspTyPheLeuLys --- LeuSerPro 135
DB 127 LeuAspTyPheLeuLys --- LeuSerPro 135
149 217 TGGATCTGATTTTGGCAATGCGATTATGCGGCAATATAGCAACAGACTTGTAAATCCA 276
QY 217 TGGATCTGATTTTGGCAATGCGATTATGCGGCAATATAGCAACAGACTTGTAAATCCA 276
DB 217 TGGATCTGATTTTGGCAATGCGATTATGCGGCAATATAGCAACAGACTTGTAAATCCA 276
150 146 ProMetLeu LeuLysGluProTyPheLysThrAlaValLeuProLeuAsnGlySerPro 154
QY 146 ProMetLeu LeuLysGluProTyPheLysThrAlaValLeuProLeuAsnGlySerPro 154
DB 146 ProMetLeu LeuLysGluProTyPheLysThrAlaValLeuProLeuAsnGlySerPro 154
151 272 TCAATTTAAAGAGATTTAAGCAATGATTTTCAATGATGATGATGATGATGATGAT 336
QY 272 TCAATTTAAAGAGATTTAAGCAATGATTTTCAATGATGATGATGATGATGATGAT 336
DB 272 TCAATTTAAAGAGATTTAAGCAATGATTTTCAATGATGATGATGATGATGATGAT 336
152 155 ArgThrProAlaArgGluLeuAsnArgSerAlaArgAlaAlaLysGluLeuGluAsnAsp 174
QY 155 ArgThrProAlaArgGluLeuAsnArgSerAlaArgAlaAlaLysGluLeuGluAsnAsp 174
DB 155 ArgThrProAlaArgGluLeuAsnArgSerAlaArgAlaAlaLysGluLeuGluAsnAsp 174
153 347 CCGTGC --- 342
QY 347 CCGTGC --- 342
DB 347 CCGTGC --- 342
154 175 ThrArgThrThrGluValLeuGlyLysGluHisGluCysAsnLeuAspGluValLysAsn 194
QY 175 ThrArgThrThrGluValLeuGlyLysGluHisGluCysAsnLeuAspGluValLysAsn 194
DB 175 ThrArgThrThrGluValLeuGlyLysGluHisGluCysAsnLeuAspGluValLysAsn 194
155 343 --- ALCATTGTGATGAGAAATGATGAGAAATGATGAGAAATGATGAGAAATGAGAA 356
QY 343 --- ALCATTGTGATGAGAAATGATGAGAAATGATGAGAAATGATGAGAAATGAGAA 356
DB 343 --- ALCATTGTGATGAGAAATGATGAGAAATGATGAGAAATGATGAGAAATGAGAA 356
156 195 Val --- TyrPheLysAsnProPheLeuProPheMetAsnSerLeuGlyLeuValThr 211
QY 195 Val --- TyrPheLysAsnProPheLeuProPheMetAsnSerLeuGlyLeuValThr 211
DB 195 Val --- TyrPheLysAsnProPheLeuProPheMetAsnSerLeuGlyLeuValThr 211
157 497 ATAAAGGAGAGATTTAAAGCAATATATTTCAAAAGCTCTTCAAGGAGATATATAAA 456
QY 497 ATAAAGGAGAGATTTAAAGCAATATATTTCAAAAGCTCTTCAAGGAGATATATAAA 456
DB 497 ATAAAGGAGAGATTTAAAGCAATATATTTCAAAAGCTCTTCAAGGAGATATATAAA 456
158 212 SerAsnGlyLeuProGluValGluAsp --- LeuSerLysAsp 224
QY 212 SerAsnGlyLeuProGluValGluAsp --- LeuSerLysAsp 224
DB 212 SerAsnGlyLeuProGluValGluAsp --- LeuSerLysAsp 224
159 477 GATTAATGCTCTGATGATTTAAAGTTTACTATATATAGCAACAGATGATAGAGAG 516
QY 477 GATTAATGCTCTGATGATTTAAAGTTTACTATATATAGCAACAGATGATAGAGAG 516
DB 477 GATTAATGCTCTGATGATTTAAAGTTTACTATATATAGCAACAGATGATAGAGAG 516
160 225 TyrThrGluLeuGlyLysGluAspLeuAspAlaArgLeuPheLeuAspHisAsp 244
QY 225 TyrThrGluLeuGlyLysGluAspLeuAspAlaArgLeuPheLeuAspHisAsp 244
DB 225 TyrThrGluLeuGlyLysGluAspLeuAspAlaArgLeuPheLeuAspHisAsp 244
161 517 TATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
QY 517 TATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
DB 517 TATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
162 245 LysThrLeuGluThrAspSerLeuAspSerPheGluThrGluArgThrProArgLys --- 263
QY 245 LysThrLeuGluThrAspSerLeuAspSerPheGluThrGluArgThrProArgLys --- 263
DB 245 LysThrLeuGluThrAspSerLeuAspSerPheGluThrGluArgThrProArgLys --- 263
163 508 --- GATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609
QY 508 --- GATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609
DB 508 --- GATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609
164 204 --- SerAsnLeuAspGluValAsnVal --- IlePro 274
QY 204 --- SerAsnLeuAspGluValAsnVal --- IlePro 274
DB 204 --- SerAsnLeuAspGluValAsnVal --- IlePro 274
165 610 ATCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669
QY 610 ATCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669
DB 610 ATCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669
166 275 ProHis --- 276
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DB 275 ProHis --- 276
167 670 CAGACATTTGAAAAAAGATATTTGAGAGCTTCTAGCGCACTGAGCGGAGAGATAT 729
QY 670 CAGACATTTGAAAAAAGATATTTGAGAGCTTCTAGCGCACTGAGCGGAGAGATAT 729
DB 670 CAGACATTTGAAAAAAGATATTTGAGAGCTTCTAGCGCACTGAGCGGAGAGATAT 729
168 277 --- ThrProValArgThrValMetAsnThrThrLeuGluLeu 288
QY 277 --- ThrProValArgThrValMetAsnThrThrLeuGluLeu 288
DB 277 --- ThrProValArgThrValMetAsnThrThrLeuGluLeu 288
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DB 710 TTAACAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789
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DB 289 LeuMetMetIleLeuAsnSerAlaSerAspLeuProSerGluLeuLeuSerTyPhe 308
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QY 790 TTAACAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 849
DB 790 TTAACAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 849
172 909 AsnAspGlyThrValAspProGlyGluSerIleLeuLysArgValLysAspIleGlyTyr 328
QY 909 AsnAspGlyThrValAspProGlyGluSerIleLeuLysArgValLysAspIleGlyTyr 328
DB 909 AsnAspGlyThrValAspProGlyGluSerIleLeuLysArgValLysAspIleGlyTyr 328
173 850 GAACTGTGTGTGTAATGCTGTGTAATGCTGTGTAATGCTGTGTAATGCTGTGTAAT 909
QY 850 GAACTGTGTGTGTAATGCTGTGTAATGCTGTGTAATGCTGTGTAATGCTGTGTAAT 909
DB 850 GAACTGTGTGTGTAATGCTGTGTAATGCTGTGTAATGCTGTGTAATGCTGTGTAAT 909

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QY 329 IlePheLysGluLysPheAlaLysAlaValGlyGlu --- GlyCysValGluIle 445
DB 329 IlePheLysGluLysPheAlaLysAlaValGlyGlu --- GlyCysValGluIle 445
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QY 910 ACTTTCCTCAACACTATACCTCAACAAACACACACACACACACACACACACTTT 969
DB 910 ACTTTCCTCAACACTATACCTCAACAAACACACACACACACACACACACTTT 969
346 GlySerGluArgTyLysLeuGlyValAlaGluTyTyArgValMetGluSerMetLeu 465
QY 346 GlySerGluArgTyLysLeuGlyValAlaGluTyTyArgValMetGluSerMetLeu 465
DB 346 GlySerGluArgTyLysLeuGlyValAlaGluTyTyArgValMetGluSerMetLeu 465
970 GCTGTAACAGACTTAAGCTGGAGAAATTTGTATATATAAATATAGTAGAGTTGTAATG 1029
QY 970 GCTGTAACAGACTTAAGCTGGAGAAATTTGTATATATAAATATAGTAGAGTTGTAATG 1029
DB 970 GCTGTAACAGACTTAAGCTGGAGAAATTTGTATATATAAATATAGTAGAGTTGTAATG 1029
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QY 366 LysSerGluGluGluArgLeuSerIleGluAsnHisSerLysLeuLeuAspAsnIle 485
DB 366 LysSerGluGluGluArgLeuSerIleGluAsnHisSerLysLeuLeuAspAsnIle 485
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QY 1030 GTTCAGAAACACCAAGACTTCACGAAATGCAATGACAGCTCTTATACAGCAAGATA 1089
DB 1030 GTTCAGAAACACCAAGACTTCACGAAATGCAATGACAGCTCTTATACAGCAAGATA 1089
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DB 486 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTySerAlaSer 405
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DB 406 ThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheProIleLeuLeuValLeu 425
1144 --- TCACCTGCTGACTTTTCTTGAGATTTTAAAGTTCTC 1179
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DB 426 AsnLeuLysAlaPheAspPheTyLysValIleGluSerPheIleLysAlaThrIleLys 445
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QY 1240 CTCCTCAAGGAGACATGCTCAACACACTAAACAGATGCAAGACACAGATTTGAGAGATTTA 1299
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466 AlaThrLeuSerAspSerProLeuPheAspLeuIleLysGluSerLysAspArg --- 483
QY 466 AlaThrLeuSerAspSerProLeuPheAspLeuIleLysGluSerLysAspArg --- 483
DB 466 AlaThrLeuSerAspSerProLeuPheAspLeuIleLysGluSerLysAspArg --- 483
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DB 483 --- 483
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DB 483 --- 483
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DB 483 --- 483
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DB 483 --- 483
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DB 483 --- 483
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QY 483 --- 483
DB 483 --- 483
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QY 1660 TCAAGCATTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1719
DB 1660 TCAAGCATTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1719
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QY 484 --- 497
DB 484 --- 497
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QY 498 --- 508
DB 498 --- 508
1777 GCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1836
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DB 509 MetTyLeuSerProVal --- ArgSerProLys 519
1847 AAGCTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1894
QY 1847 AAGCTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1894
DB 1847 AAGCTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1894
520 LysGlySerThrThrAlaValAsnSerIleAlaAsnAlaGluThrGluAlaThrAla 539
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DB 520 LysGlySerThrThrAlaValAsnSerIleAlaAsnAlaGluThrGluAlaThrAla 539
1844 --- 1945
QY 1844 --- 1945
DB 1844 --- 1945
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13 560 LeuGluHisIleIleIleThrLeuPheGluHisThrLeuGluAsnGluTyrGluLeuMet 599
14 2047 TTAAGAAAGCAATAGCAAGGCTGCTTCAAACTTACTTACACCTGGCTGCTGCTGCTGCT 2106
15 600 ArgAspArgHisLeuAspGluIleMetMetCysSerMetTyrGlyIleCysLysValLys 619
16 2107 AAAAGAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2166
17 620 AsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaVal 639
18 2167 AAAAGAAAGAAATTTTAAAGATATGAAAGATATGAAAGATATGAAAGATATGAAAGAT 2226
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21 649 ----- 649
22 2287 AAAAATAAATATATATATATATATATATATATATATATATATATATATATATATATAT 2346
23 650 -----GluGluGluTyrAspSerIleIleValPheLysAsn 661
24 2447 CTTGATGCTTTCATGCAAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2406
25 662 SerValPheMetGluArgLeuLysThrAsnIleLeuGluThrAlaSerThrArg----- 679
26 2407 ACAAATAATATAGCAAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2466
27 680 -----ProProThrLeuSerPheIleProHisIleProArgSerProTyrLys 695
28 2467 CATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2517
29 696 PheProSerSerProLeuArgIle ProGlyGlyAsnIleTyrIleSerProLeuLys 714
30 2518 -----CATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2562
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32 2563 CCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2604
33 745 IleLeuValSerIleGlyGluSerProGlyThrSerGluLysPheGluLysIleAsnGlu 754
34 2605 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2658
35 765 MetValCysAsnSerAsp-----ArgValLeuLysArgSerAlaGluGly 769
36 2659 ATATAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2718
37 770 SerAsnThrProLys 774
38 2719 GAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2733
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RESULTS

```
Sequence 1, Application US/08152721B
Patent No. 6962315
GENERAL INFORMATION
APPLICANT: Livingston, David M.
APPLICANT: Ewen, Mark E.
TITLE OF INVENTION: DNA Encoding p107 Tumor Suppressor and
Related Polypeptides
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL & STEWART
STREET: 54 State Street
CITY: Boston
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STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,721B
FILING DATE: 15-Nov-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pasternack Esq., Sam
REGISTRATION NUMBER: 29,576
REFERENCE/DOCKET NUMBER: 181411-011DIV
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2808 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: cDNA encoding p107
US-08-152-721B-1
Alignment Scores:
Prod. No. Length Score
55 LeuLeuLysLysTyrValLeuPheAla-----LeuPheSer----- 67
67 4 ATATCAAAATAATGAGCAATTTTITAGATAATTTCAAAATCCATAICAGAAACA 63
68 ---LysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSer 86
68 64 CCAAAATTACACGA-----AGGGAAGAGAGAGAGATTCT 102
87 ThrGluIleAsnSerAlaLeuValLeuLysValSerTyrIleThrPheLeuLeuAlaLys 106
103 TCCAGCTTAAAGCA-----CTGTATTAATTTCTGTCACACACTTTTCTTATACIAAG 156
107 GlyGluValLeuGlnMetGluAspSerLeuValIleSerPheGluLeuMetLeuCysVal 126
157 GGTAAATTTCCGATGATGAGGATGACITAGTAAACTCTATCATTTACTTCTATCTCC 216
127 LeuAspTyrIleLys-----LeuSerPro 135
217 TCGATCTGATTTTCCCAATGCGATTATGCGCAATATGACAAATTTGTTAAATGCA 276
136 ProMetGln LeuLysGluProTyrLysThrAlaValIleProHisAsnTyrSerPro 154
277 TCAATTAAGGCTTACCATCTGATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336
155 ArgThrProArgArgGlyGlnAsnArgSerAlaValIleAlaLysIleLeuLeuAsnAsp 174
337 CCTGCT----- 342
175 ThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspIleValLysAsn 194
343 -----ATCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 396
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 1450 AACAACTAAAGAAATGTTGAAATATATCTCAGCATTTCCAGCCAGAGGATTC 1509
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 1510 AATAAATGCTGAAACAAATCCAGCAACAACTTTCGTTTGGGAGCATCTTTACTAT 1569
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 479 LysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaIleGluValVal 398
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 1780 TTATATAGAGAGAAATGAGCTTTTGTAGAGAGTGGTAAATGAAATGAAATGAAATGAA 1849
 459 HisArgIleMetGluSerLeuAlaIlePheLeuSerAspSerProLeuPheAspLeuIleLys 478
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 Db 2500 TCTCAACAGGTGACAGGAACAATTTCAGAGTCCAGGTTAAAGTGGATTCATTCACAGAT 2559
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 Db 2560 AGCAACACAGCTCTTATTCAGGAGGAGCAATTCAGAGAGATACCAATTCAGAGAGATTC 2619
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 Db 2620 CTTCGGAGATCTCTGAGGAAATAGATATTCAGAT-----GAATTCAGAGAGAGAGAGAT 2674
 QY 585 TTTTThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAlaHisLeu 604
 Db 2674 TGGACCTGCTTGAATTCCTCATATTCAGTCTCTCTGAAATTCATGATGAGAGAGATCTG 2744
 QY 605 AspGlnIleMetLysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 624
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10 3421 GCGACAAAAATCCTGCTTATTAAGCGCTGCTGTAATATGATGTAATGCT 3477
RESULT 15
US-09-026-459a-35
Sequence 1, Application: US-09-026-459a-35
Patent No. 5840506
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 116
PUBLICATION/REFERENCE ADDRESS:
AUTHOR/INVENTOR: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILED BY: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/842,877
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 40,486
REFERENCE/DEPOSIT NUMBER: 8321-13 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4853 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 70 4899
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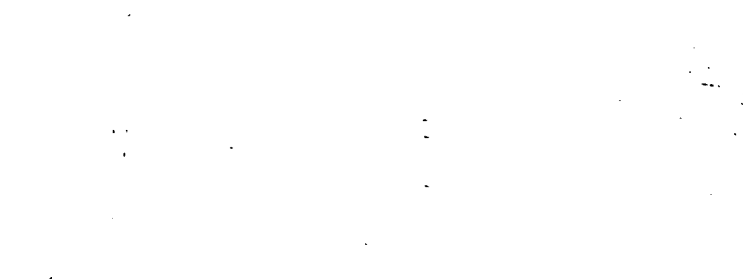
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RESULT 5

US 08-959-638-7

Sequence 7, Application: us-09-026-459a

Patent No. 5932210

GENERAL INFORMATION:

APPLICANT: Gregory, Richard J.

APPLICANT: Wills, Ken N

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1 APPLICANT: Maneval, Daniel C.
2 TITLE OF INVENTION: Recombinant Adenoviral Vector and
3 METHOD OF INVENTION: Methods of Use
4 NUMBER OF SEQUENCES: 9
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Campbell and Flores
7 STREET: 4370 La Jolla Village Drive, Suite 700
8 CITY: San Diego
9 STATE: California
10 COUNTRY: USA
11 ZIP: 92122
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent In Release #1.0, Version #1.25
17 APPLICATION DATA:
18 APPLICATION NUMBER: US/08/959,638
19 FILING DATE:
20 CLASSIFICATION:
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22 APPLICATION NUMBER: US/98/329,673
23 FILING DATE: 25-OCT-1994
24 APPLICATION NUMBER: US 08/233,777
25 FILING DATE: 19-MAY-1994
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/067,142,669
28 FILING DATE: 25-OCT-1993
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Campbell, Cathryn A.
31 REGISTRATION NUMBER: 31,815
32 REFERENCE/DOCKET NUMBER: P-CJ 1192
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (619) 535-9001
35 FAX: (619) 535-8949
36 INFORMATION FOR SEQ ID NO: 7:
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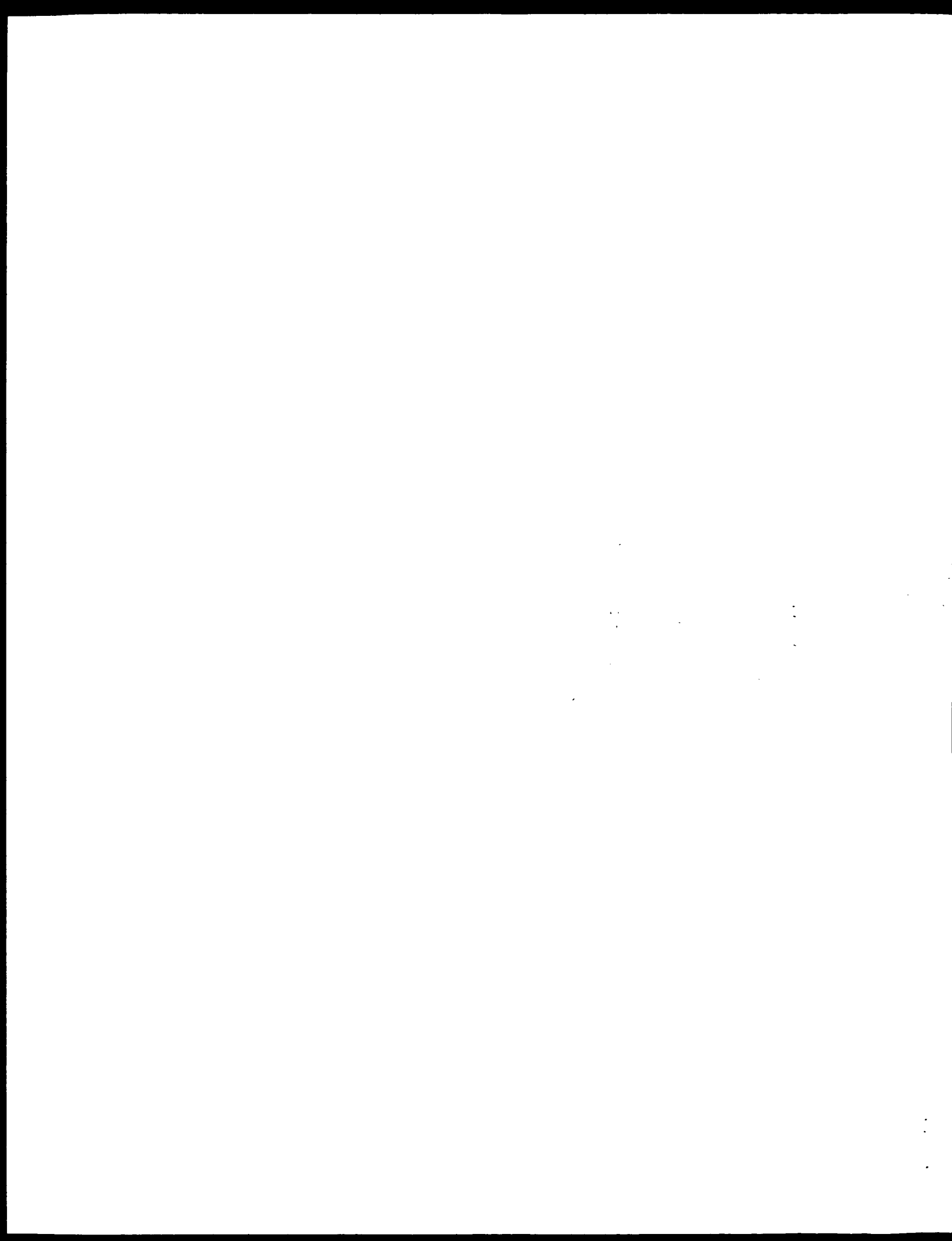
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RESULT 10
US-08-470-091-1
: Sequence 1, Application US/08470091
: Patent No. 5912236
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: APPLICANT: Hu, Shi Xue
: APPLICANT: Benedict, William F.
: TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
: TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10016-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/470,091
: FILING DATE: JUN-16-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/038,760
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Polissant, Brian M
: REGISTRATION NUMBER: 28,462
: REFERENCE/DECKET NUMBER: 7139-025 339
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3232 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 19..2469
US-08-470-091-1

Alignment Scores:
Pred. No.: 0 Length: 4232
Score: 4213.00 Matches: 820
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.83% Indels: 0
DB: 2 Gaps: 0

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QY 2744 TGTGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 2802
DB 2745 TGTGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 471
QY 2804 TTTGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 2862
DB 2805 TTTGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 411
QY 2864 CATATGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 2922
DB 2865 CATATGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 351
QY 2924 ATGCAACCTTTGAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 2982
DB 2925 ATGCAACCTTTGAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 291
QY 2984 ATGCAACCTTTGAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 3042
DB 2985 ATGCAACCTTTGAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 231
QY 3044 AATGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 3102
DB 3045 AATGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 171
QY 3104 TGTGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 3162
DB 3105 TGTGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 111
QY 3164 TATGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 3222
DB 3165 TATGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 51
QY 3224 TTTGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 3286
DB 3225 TTTGCTTTTAAATGCTTTTCCGATGCTTTGAAATGCTTTGAAATGCTTTGAAATGCTTT 7

14 1870 GACGAGAGAGGACCAATGATACGCTTGAATCTCTTGTCTCTTAATCTCTCTCTCCAG 1929
15 1510 AATAAATAC 1569
16 1940 AATAATAC 1989
17 1570 TCAATCAAGGCTTAAATTTATCTCAATATGATGATGATGATGATGATGATGATGATG 1629
18 1990 CAAATACAGGCTTAAATTTATCTCAATATGATGATGATGATGATGATGATGATGATG 2049
19 1630 AAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1689
20 2060 ACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2109
21 1690 GCGTACGCGGCTTAAATTTATCTCAATATGATGATGATGATGATGATGATGATGATG 1749
22 2110 GCGTACGCGGCTTAAATTTATCTCAATATGATGATGATGATGATGATGATGATGATG 2169
23 1750 CATATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1809
24 2170 CATATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2229
25 1830 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1869
26 2240 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2289
27 1870 GACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1929
28 2290 GACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2349
29 1930 ACATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1989
30 2450 ACATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2409
31 1990 TCGCTCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2049
32 2410 TCGCTCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2469
33 2050 ACCTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2109
34 2470 ACCTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2529
35 2110 GAGATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2169
36 2530 GAGATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2589
37 2170 GAGATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2229
38 2590 GAGATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2649
39 2230 ICATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2289
40 2650 ICATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2709
41 2290 GTGCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2349
42 2710 GTGCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2769
43 2450 GATATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2409
44 2770 GATATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2829
45 2410 GAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2469
46 2830 GAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2889
47 2470 GATATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2529
48 2890 GATATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2949
49 2530 TGTGTACAGGCTTCGATTCATCTCTCTCACAGATGCTGAT 2574
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Db 2956 TGTGTACAGGCTTCGATTCATCTCTCTCACAGATGCTGAT 2994

RESULT 6

US-08-482-627-4
Sequence 4, Application US/08482627
Patent No. 5998134
GENERAL INFORMATION:
APPLICANT: Lec, Won-Hwa
APPLICANT: Lec, Eva Y-H.P
TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
TITLE OF INVENTION: and Regulator
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,627
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,947
FILING DATE: 28-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1707
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION POP SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 139..2924
US-08-482-627-4

Query Match 78.5%; Score 2565; DB 2; Length 2994;
Best local similarity 100.0%; Pred. No. 0;
Matches 2565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTGTGGGAGATCTATCTTTATTCAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 69
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Db 430 CTGTGGGAGATCTGATCTTTATTCAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 489
QY 70 ACTGAGTACAGAAAAACATAGAAATCAGCTGCTCCATAAATTCCTTTAACTTACTTAAAGAA 129
|||||
Db 490 ACTGAGTACAGAAAAACATAGAAATCAGCTGCTCCATAAATTCCTTTAACTTACTTAAAGAA 549
QY 130 ATTGATACCAAGTACCAAGCTGATAATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 189
|||||
Db 550 ATTGATACCAAGTACCAAGCTGATAATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 609
QY 190 TTTTTCATCTTTTATCTTTATCTTTATCTTTATCTTTATCTTTATCTTTATCTTTATCT 249
|||||
Db 610 TTTTTCATCTTTTATCTTTATCTTTATCTTTATCTTTATCTTTATCTTTATCTTTATCT 669
QY 250 ACCAGTTCGATATCTACTCAAAATTAATTCGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 309
|||||
Db 670 ACCAGTTCGATATCTACTCAAAATTAATTCGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 729

1570 AATGCAAAATTTTTCATATGCTTTTATGCGGTCGCGCTGAGGCTGTAATGGCCACA 1629
1580 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1269
1590 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1269
1600 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1689
1610 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1689
1620 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1329
1630 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1749
1640 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1389
1650 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1809
1660 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1449
1670 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1869
1680 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1509
1690 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1929
1700 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1569
1710 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1989
1720 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1629
1730 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2049
1740 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1689
1750 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2109
1760 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1749
1770 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2169
1780 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1809
1790 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2229
1800 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1869
1810 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2289
1820 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 1929
1830 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2349
1840 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2049
1850 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2369
1860 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2089
1870 TATATGAAATATGATCTCGAATCTGATCTGGAAAGATTTGCTTTTTCATGATAT 2709

2240 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2349
2250 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2769
2260 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2769
2270 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2409
2280 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2829
2290 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2469
2300 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2889
2310 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2529
2320 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2949
2330 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2574
2340 GTCTCAAAACAACTGCGGGAAGGACCAAGCGCTCCCTAAAGCACTCAAAAATTAQNT 2994

RESULT 10

US-08-959-638-7
Sequence 7, Application US/08959638
Patent No. 5932210
GENERAL INFORMATION:
APPLICANT: Gregory, Richard J.
APPLICANT: Willis, Ken N.
APPLICANT: Mancini, Daniel C.
TITLE OF INVENTION: Recombinant Adenoviral Vector and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenting Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT NUMBER: US, 08, 959, 638
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICANT NUMBER: US, 08, 959, 638
FILING DATE: 25-OCT-1994
APPLICATION NUMBER: US 08/233,777
FILING DATE: 19-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Kathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P. 01, 1192
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2995 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 139..2922

1 APPLICATION NUMBER: 09/106,494
2 FILING DATE: August 12, 1993
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Monaco, Daniel A.
5 REGISTRATION NUMBER: 40,480
6 REFERENCE/DOCKET NUMBER: 6056 188 D11
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (215) 568-8483
9 TELEFAX: (215) 568-8484
10 INFORMATION FOR SEQ ID NO: 1:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 3249 base pairs
13 TYPE: nucleic acid
14 STRANDEDNESS: Single
15 TOPOLOGY: Linear
16 US 08 429 264 1

Query Match 2.1% Score 68.2; DB 1: Length 4249;
Best Local Similarity 53.0%; Pred. No. 1.5e 06;
Matches 170; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 1634 AAAAAATTGAAATCTATCTCTTTTACATGCTTTTATAAAAAAGTGATGGGTAGGCT 1693
DB 2412 ATAGACACAGACAGACAGCTCTTTATGCTTTCTTTAGAAAGTATACCATTTAGCAG 2371
QY 1694 AATCGGGTAAATATCTTTGAAAGCTTCTGCTGAGCAGCAGCAATTAGAACATA 1753
DB 2472 CTGTGGGCTTGGAGATCTGTG---GCAAACTAGATATTTCATGATTTAGGAGAAA 2428
QY 1754 TAACTGGAGCTTTTTCAGACACAGCTTCCAGAAAGTATGATCAATCAAGACACAGAC 1813
DB 2429 AATCTGAGAGCTTTTAACTCTGATTAATTCAGTCTGCACTTATGATGAGACAGAC 2488
QY 1814 ATTGAGCAAAATATGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1873
DB 2489 AATCTGAGAGCTTTTAACTCTGATTAATTCAGTCTGCACTTATGATGAGACAGAC 2548
QY 1874 TAAATTCAAATCATTTAAACAGATATACAGATATACAGATATACAGATATACAGATAT 1933
DB 2449 AATCTGAGAGCTTTTAACTCTGATTAATTCAGTCTGCACTTATGATGAGACAGAC 2608
QY 1934 TCAAAAGCTTTTTCAGTCAAAAG 1954
DB 2609 ATAGAGTGTTTTGTATAAAG 2629

RESULT 15
US 08 842 883 1
Sequence 1, Application US/08842883
Patent No. 5807681
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
APPLICANT: Baldi, Alfonso
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
TITLE OF INVENTION: OF CANCER
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIHEL, GENIA, LAVAGNA & MONACO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: pc DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,883
FILING DATE:
CLASSIFICATION: 445

1 ATTORNEY/AGENT INFORMATION:
2 NAME: Monaco, Daniel A.
3 REGISTRATION NUMBER: 40,480
4 REFERENCE/DOCKET NUMBER: 8421 13 US1
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: (215) 568-8483
7 TELEFAX: (215) 568-8484
8 INFORMATION FOR SEQ ID NO: 1:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 4853 base pairs
11 TYPE: nucleic acid
12 STRANDEDNESS: double
13 TOPOLOGY: Linear
14 MOLECULE TYPE: cDNA
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: 70..3489
18 US-08-842-883-1

Query Match 2.1% Score 68.2; DB 1: Length 4853;
Best Local Similarity 53.0%; Pred. No. 1.7e 06;
Matches 170; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 1634 AGAAGCCATTGAAATCTATCTCTTTTACATGCTTTTATAAAAAAGTGATGGGTAGGCT 1694
DB 2552 ATAGACACAGACAGACAGCTCTTTATGCTTTCTTTAGAAAGTATACCATTTAGCAG 2611
QY 1694 AATCGGGTAAATATCTTTGAAAGCTTCTGCTGAGCAGCAGCAATTAGAACATA 1754
DB 2612 CTGTGGGCTTGGAGATCTGTG---GCAAACTAGATATTTCATGATTTAGGAGAAA 2428
QY 1754 TAACTGGAGCTTTTTCAGACACAGCTTCCAGAAAGTATGATCAATCAAGACACAGAC 1813
DB 2669 AATCTGAGAGCTTTTAACTCTGATTAATTCAGTCTGCACTTATGATGAGACAGAC 2728
QY 1814 ATTGAGCAAAATATGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1874
DB 2729 AATCTGAGAGCTTTTAACTCTGATTAATTCAGTCTGCACTTATGATGAGACAGAC 2788
QY 1874 TAAATTCAAATCATTTAAACAGATATACAGATATACAGATATACAGATATACAGATAT 1934
DB 2789 AATCTGAGAGCTTTTAACTCTGATTAATTCAGTCTGCACTTATGATGAGACAGAC 2848
QY 1934 TCAAAAGCTTTTTCAGTCAAAAG 1954
DB 2849 ATAGAGTGTTTTGTATAAAG 2869

Search completed: January 17, 2003, 18:21:17
Job time : 109.02 secs



1 INFORMATION FOR SEQ ID NO: 2:

2 SEQUENCE CHARACTERISTICS:

3 LENGTH: 2994 base pairs

4 TYPE: nucleic acid

5 STRANDEDNESS: double

6 TOPOLOGY: linear

7 M-VALUE TYPE: DNA (cDNA)

8 SIZE: 204 329+2

9 ALIGNMENT SCORES:

10 Prod. No. 0 Length: 2994
 11 Score: 4467.00 Matches: 850
 12 Percent Similarity: 100.00% Conservative: 0
 13 Best Local Similarity: 100.00% Mismatches: 0
 14 Query Match: 99.89% Indels: 0
 15 Caps: 1

16 US 09-026-459A 33 (1-851) x US-09-026-459-2 (1-2994)

21 GlnLysValSerSerValAspGlyValLeuGlySerTyrIleGlnLysLysLysGluLeu 21
 22 TrpGlyIleCysIlePheIleAlaValAspLeuAspGluMetSerPheThrPheThr 41
 23 TGGCAATCTGATCTTATGAGAGAGAGTGAATGAGAGAGAGAGAGAGAGAGAGAG 432
 24 GAGAAAG 432
 25 TGGCAATCTGATCTTATGAGAGAGAGTGAATGAGAGAGAGAGAGAGAGAGAGAG 442
 26 GlnLeuGlnLysAsnIleGluIleSerValHisIysPheIleAsnLeuLysGluIle 61
 27 GAG 552
 28 GAG 552
 29 AspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 81
 30 CATATCAGTACCAAACTGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCA 612
 31 PheAlaLeuPheSerLysLeuGluAlaThrCysGluLeuIleTyrLeuThrGlnProSer 101
 32 TTTGGATCTTTCAGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAAT 572
 33 SerSerIleSerThrGluIleCysSerAlaLeuValIleLysValSerTrpIleThrPhe 121
 34 AGTTGATATCTATGAAATGAAATGCAAAATGCAAAATGCAAAATGCAAAATGCA 732
 35 LeuLeuAlaLysGlyGluValLeuGlnMetGluAspLeuValIleSerPheGlnLeu 141
 36 TATAGCAAAAG 792
 37 MetLeuGlyValLeuAspTyrPheIleLysLeuSerProPheMetLeuLysGluPro 161
 38 AGTATGATCTTTCAGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAA 852
 39 TyrLysThrAlaValIleProIleAsnGlySerProArgThrProArgGlyGlnAsn 181
 40 TATATAAG 912
 41 ArgSerAlaAlaIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCys 201
 42 AG 972
 43 LysAlaHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePro 221
 44 AAAG 1032
 45 PheMetAsnSerLeuGlyLeuValThrSerAspGlyLeuProGluValGlnAsnLeuSer 241
 46 TTTATGAG 1092
 47 LysArgTyrGlnIleIleTyrLeuLysAsnLysAspLeuAspAlaAlaLeuPheLeuAsp 261
 48 AAAG 1152
 49 HisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 281
 50 TTTATGAG

1153 CATGATAAATCTCTTCAACATGATCTTATGAGAGAGAGAGAGAGAGAGAGAG 1212
 1213 AAAAGTAACTTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1272
 1313 AATCTGATTTCTGATTTTAACTGATGATGATGATGATGATGATGATGATGATGAT 1392
 1413 GTCCAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512
 1513 TCTATGATTTAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1572
 1613 ACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692
 1713 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1792
 1813 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1872
 1913 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1992
 2013 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2092
 2113 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2192
 2213 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2292
 2313 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2392
 2413 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2492
 2513 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2592
 2613 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2692
 2713 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2792
 2813 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2892
 2913 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2992

QY 222 PheMetAsnSerLeuLeuValThrSerAsnGlyLeuProGluValGluAsnLeuSer 241
DB 1044 LTHAIGAAATTCCTGGACATCTGAACAATCTAATGGACTCCAGAGCTCAAAATCTTCT 1092
QY 242 LysAlaGlyGluGlnIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAsp 261
DB 1045 AAANATAGCAAGAAATTTATCTTAAANATAAANATATAGATGCAAGATTAATTTGGAT 1152
QY 262 HisAspLysThrLeuGlnThrAspSerLeuAspSerPheGluThrGlnArgThrProArg 281
DB 1046 CATGATAAAATCTCTCACTGATGATCTATAGACAGATTTGAAACACAGCAACACAGCA 1212
QY 282 LysSerAsnLeuAspGluGluValAsnValIleProProHisThrProValArgThrVal 301
DB 1214 AAAAGTAACTTCAAGACAGGCAAGATTAATTCCTCCACACATCCAGCTTACGACTGTT 1272
QY 302 MetAsnThrIleGlnIleGlnMetMetMetMetMetMetMetMetMetMetMetMetMet 321
DB 1274 ATGAAACATATCCAAACAAATTAATGATGATTTAAATTCAGCAAGTATACGCTTCAGAA 1332
QY 322 AsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArg 341
DB 1334 AAATGCAATTCCT 1392
QY 342 ValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnLysCys 361
DB 1394 GTCAGCAATATAGCAATATCTTAAACAGCAAAATTTCTTAAAGCTTCGCGACAGCTTCT 1452
QY 362 ValGlnIleGlySerGlnArgTyrTyrLysGlyValArgLysTyrTyrArgValMetGlu 381
DB 1454 GTCAAAATTTGATGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1512
QY 382 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsn 401
DB 1514 TCCATGCTTAAATCAGAAAGAAAGCAATATCCATTCATCAAAATTTTACGAAACCTGCAAT 1572
QY 402 AspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyr 421
DB 1574 GACAAATTTTCAATGCTGATATGCGCGTGGCTGAGCTGCTGATGCGCAATAT 1632
QY 422 SerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIleLeu 441
DB 1634 AGCAGAAATACATCTCAATCTTCTGATTTCTGAAACAGATTTCTTCCCATGCTGCTG 1692
QY 442 AsnValIleAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAla 461
DB 1694 AAAGCTTAAATTTAAAGGCTTTCATTTTACAAAGCTGATCAAAAGCTTTTATCAAGCA 1752
QY 462 GluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMet 481
DB 1754 GAAAGCAATTCACAGAGAGAAATCAAAACATTTAGACCAATTCGACATCGAAATCATG 1812
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QY 742 LeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSer 761
DB 2594 CTGCTCAATCTCAACAAACAAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCT 2652
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QY 782 LeuLysArgSerArgGluGlySerAsnProGlySerPheGluLysLysLeuArgPheAsp 801
DB 2714 CTGTAATCTTTGTAATCTTTGTAATCTTTGTAATCTTTGTAATCTTTGTAATCTTTGTAAT 2772
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RESULT 3

US-08-801-092-3
: Sequence 3, Application US/08061092
: Patent No. 6074850
: GENERAL INFORMATION:
: APPLICANT: Antelman, Douglas
: APPLICANT: Gregory, Richard J.
: APPLICANT: Mills, Kenneth N.
: TITLE OF INVENTION: Tissue Specific Expression of
: RETINOBLASTOMA PROTEIN
: NUMBER OF SEQUENCES: 46
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111

1 COMPILER RELEASABLE FORM:
 2 MEDIUM TYPE: Floppy disk
 3 COMPUTER: IBM PC compatible
 4 OPERATING SYSTEM: PC DOS/MS DOS
 5 SOFTWARE: Pattern In Release #1.0, Version #1.00
 6 CURRENT APPLICATION DATA:
 7 APPLICATION NUMBER: 09-026-459a-33
 8 FILING DATE: 14 FEB 1997
 9 CLASSIFICATION: 514
 10 PRIOR APPLICATION DATA:
 11 APPLICATION NUMBER: 09-08751-517
 12 FILING DATE: 15 NOV 1996
 13 CLASSIFICATION: 514
 14 ATTORNEY/AGENT INFORMATION:
 15 NAME: Fitts, Robert A.
 16 REGISTRATION NUMBER: 45,146
 17 REFERENCE/POCKET NUMBER: 316940 091020
 18 TELECOMMUNICATION INFORMATION:
 19 TELEPHONE: 415-576-0200
 20 TELEFAX: 703-576-0300
 21 INFORMATION FOR SEQ ID NO: 1:
 22 SEQUENCE CHARACTERISTICS:
 23 LENGTH: 2994 base pairs
 24 TYPE: nucleic acid
 25 STRANDEDNESS: single
 26 TOPOLOGY: linear
 27 MOLECULE TYPE: cDNA
 28 US 08 801 092 3

Alignment Scores:
 1 Prod. No.: 0 Length: 2994
 2 Score: 4467.00 Matches: 850
 3 Percent Similarity: 100.00% Conservative: 0
 4 Best Local Similarity: 100.00% Mismatches: 0
 5 Query Match: 99.89% Indels: 0
 6 Gaps: 0

US 09 026 459a-33 (1 851) x US 08 801-092 3 (1-2994)

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 QY 22 TrpPylIleCysIlePheIleAlaValAspLeuAspGluMetSerPheThrPheThr 41
 DB 433 TGGGAATCTGTATCTTATTTCAGACGTTGACCTAGAGATGATGCTGCTTACT 452
 QY 42 GlnLeuGlnLysAsnIleGlnIleSerValHisLysPheAsnLeuLeuLysGluIle 61
 DB 494 GATATACACAAAGACAAACAAATACAGTGGCAATATTTTAACTTACAAAAGAAAT 552
 QY 62 AspThrSerThrLysValAspAspAlaMetSerArgLeuLeuLysLysGlyTyrAspValLeu 81
 DB 554 GATATACATCAAAAGCTTCAATATGCTATGCTATGCTATGCTATGCTATGCTATG 612
 QY 82 PheAlaIlePheSerThrLysLeuAlaArgThrCysGlnLeuIleTyrIleThrGlnProSer 101
 DB 613 TTGACTCTTCAGCAATATGAAAGACATGTAATTTATATATTTGACAAACACAGC 672
 QY 102 SerSerIleSerThrGlnIleAsnSerAlaLeuValIleLysValSerTrpIleThrPhe 121
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 QY 122 LeuLeuAlaLysGlyGlnValLeuGlnMetGlnAspAspLeuValIleSerPheGlnLeu 141
 DB 733 TATATACATAAGAGCAATATCAAAAGCAATATATATATATATATATATATATAT 792
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 QY 182 ArgSerAlaArgIleAlaLysLeuLeuAlaAspThrArgIleIleLeuValLeuGlySer 201
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 DB 1333 AATCTGATTCCTATTTTAACTGACAGTGAATATATATATATATATATATATATATAT 1392
 QY 342 ValLysAspIleGlyTyrIlePheLysGlnLysPheAlaLysAlaValIleGlnGlyCys 361
 DB 1393 GTCAAGCATATAGCAT 1452
 QY 362 ValGlnIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGln 381
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 DB 1573 GACAACTATATCAAT 1632
 QY 422 SerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIleLeu 441
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 QY 462 GlnGlyAsnLeuThrArgGlnMetIleLysHisGlnGlnArgCysGlnHisArgIleMet 481
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 DB 1813 GAATGCTTAAAT 1872
 QY 502 ArgGlnGlyProThrAspHisLeuLeuSerAlaCysProLeuAsnLeuProLeuHis 521
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RESULT 6
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; Sequence 1, Application PC/TUS9410357
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
; TITLE OF INVENTION: Susceptibility Gene Product
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER PEAKABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10357
; FILING DATE: 13-Sep 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,108
; FILING DATE: 13-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: EP 06 1117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9601
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; NAME/KEY: CDS
; LOCATION: 1..2923
PCT-US94-10357-1
Alignment Scores:
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Score: 4364.00 Matches: 849
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.88% Mismatches: 0
Query Match: 99.82% Indels: 0
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US-09-026-459A-33 (1-851) x PCT-US94-10357 1 (1-2994)

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27 782 LeuLysSerThrLysThrLysThrLysThrLysThrLysThrLysThrLysThr 801
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RESULT 7
US 08 428 674A 7
Sequence 7, Application US/08428674A
Patent No. 6210949
GENERAL INFORMATION:
APPLICANT: Gregory, Richard J.
Wills, Ken N.
TITLE OF INVENTION: Recombinant Adenoviral Vector and Methods of Use
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-0848
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,674A
FILING DATE: 25 Oct 1994
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25 Oct 1994
APPLICATION NUMBER: US 08/244,669
FILING DATE: 25 Oct 1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy S.
REGISTRATION NUMBER: 35,367
REFERENCE/PATENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2945 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MODULE TYPE: CDS

FEATURE:
NAME/KEY: CDS
LOCATION: 139..2925
OTHER INFORMATION: /product= "RB"
/note= "relinblastoma tumor suppressor"
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-328-674A-7
Alignment Scores:
Pred. No.: 0 Length: 2995
Score: 4357.00 Matches: 849
Percent Similarity: 99.88% Conservatives: 0
Best Local Similarity: 99.88% Mismatches: 3
Query Match: 99.66% Indels: 0
DB: 4 Gaps: 0
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Db 433 TGGGAAATCTGTAATCTATTCACACAGCAGTACAGTACAGTACAGTACAGTACAG 492
QY 42 GluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysLeuIle 61
Db 493 GAGCTACAGAAAAATACAAATACATGATGATGATGATGATGATGATGATGATGATG 552
QY 62 AspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysLysLysLys 81
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Db 673 AGTTGATATCTACTGAAATAAATTTCTGATGATGATGATGATGATGATGATGATGAT 732
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QY 182 ArgSerAlaArgGluAlaLysGlnLeuGluAsnAspThrArgIleLeuValLeuLys 201
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1 REGISTRATION NUMBER: 26,462
 2 REFERENCE/PROJECT NUMBER: 7409 026-999
 3 TELECOMMUNICATION INFORMATION:
 4 TELEPHONE: (212) 793 9999
 5 TELEFAX: (212) 869 9741/8864
 6 TELEX: 66141 PENNIE
 7 INFORMATION FOR SEQ ID NO: 1:
 8 SEQUENCE CHARACTERISTICS:
 9 LENGTH: 3242 base pairs
 10 TYPE: NUCLEIC ACID
 11 STRANDEDNESS: double
 12 ORIENTATION: not relevant
 13 MOLECULE TYPE: DNA
 14 FEATURE:
 15 NAME/KEY: CDS
 16 LOCATION: 19..2459
 17 US 08 038 740 1

Alignment Scores:

Prod. No.: 0 Length: 4242
 Score: 4214.00 Matches: 820
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.46% Indels: 0
 Gaps: 1

US 09 026 459A 33 (1 851) x US 08 038 760-1 (1-1242)

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 61 CATAAATCTTAAATTGATTAATAAGAAATTCATACACCAAAAGTTGATAATGCTATG 126
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 92 CysGluLeuLeuTyrrLeuThrGlnProSerSerLeuSerThrGluLeuAsnSerAla 111
 187 TGTCAACTTATAATATCACAAACCCAGCACTTCGATATCTACTGAAAATAATCTGCA 246
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1 ATTENTION NUMBER: US/09/038,760
 2 FILING DATE:
 3 AGENCY/AGENCY INFORMATION:
 4 NAME:
 5 REGISTRATION NUMBER: 28,462
 6 REFERENCE/KEY NUMBER: 7400 026 900
 7 TELEPHONE: (212) 740-0000
 8 TELEPHONE: (212) 740-0000
 9 TELEPHONE: (212) 740-0000
 10 TELEPHONE: (212) 740-0000
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Alignment Scores:
 1 Predicted: 3240
 2 Score: 4213.00
 3 Percent Similarity: 100.00%
 4 Best Local Similarity: 100.00%
 5 Query Match: 96.36%
 6 Indels: 0
 7 Caps: 0

US-09-026-459A-33 (1 851) x US-08-470-091-1 (1-3232)

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607 AATGSAVTPCAAGAGGIIAGAAALIIIICTAAAGATAGAGAAATTTATCTTAAAT 666
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RESULT 12
US-07 708 952-1
Sequence 1, Application US/07708962
Patent No. 5,263,321
GENERAL INFORMATION:
APPLICANT: Livingston, David M.
APPLICANT: Ewen, Mark E.
TITLE OF INVENTION: Tumor Suppressor
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate, Hall & Stewart
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

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 QY 398 LysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaLysAlaLeuGluValVal 417
 DB 1640 GATAATGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1689
 QY 418 MetAlaThrTyrSerArgSerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPhe 437
 DB 1690 ATATGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1719
 QY 438 ProPheIleLeuAsnValLeuAsnLeuLysAlaPheAspPheCylLysValIleGluSer 457
 DB 1720 GATATGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1779
 QY 458 PheIleLysAlaGluLysLeuArgLeuArgLeuMetIleLysHisLeuGluArgCysGlu 477
 DB 1780 ATATGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1839
 QY 478 HisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuLys 497
 DB 1840 GAAATGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1899
 QY 498 GluSerLysAspArgLeuThr... ProThrAspHisLeuGluSer 511
 DB 1900 GATATGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1959
 QY 512 Ala... CysProLeuAsnLeuProLeuGluAsnAsnHis... 523
 DB 1960 GATATGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2019
 QY 524 ThrAlaAlaAspMetTyr... 529

DB 2020 GGTATATGAGAGATTGAGAGAGATATAATATCTCAATATATAAGAGAGAT 2079
 QY 530 LeuSerProValArgSerProLysLys... 539
 DB 2080 AGCTGCTCAATGAGCAGAGATAGTACAGAGAGGCGGTATTGTGTGCAATGATAGAGCTCT 2149
 QY 539 549
 DB 2140 GATGAGGAGCGCTGGCGGCAATGCGGCAAGCGGCTAGTCAATGCTGCTGCTGCTGCTGCT 2199
 QY 540 GlySerThrArgValAsnSer... 547
 DB 2200 AATGATATGCGGAGAGCTGCTGCTGCAATGAGTTTGGATATCTTGGTATGATG 2259
 QY 548 ThrAlaAsn... 550
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 QY 551 AlaGluThr 554
 DB 2320 GCTAAATGAAAAATGCAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2379
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 QY 560 560
 DB 2440 TCTCAACAGTGATGAGAGCAATTTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2499
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34  ProLeuLysLysLeuArgPheAspPheLeuGlySerAspGluAlaAspLysSerLysHis 813
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
36  GCATCTAAACACAGACGAAATCTTTTGGAAAGATCGAATCACCCTGCAAAAGCAATT 3420
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
38  LeuPro GlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArg 831
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
40  TGGCAGAAAATCATTCGTGCTTATTACGGGGCTGCAAGATGTAGCTAATGACGT 3477
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Search completed: January 19, 2003, 05:23:02
CPU time : 156.41 secs

QY 420 GACAGTCTTGAACACACAGAACACACAGGAAAGTAACTTTCATGACAGAGGTAAGTGA 879
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QY 480 ATTGCTGACACAGTCCAGTTCAGGACCTTATGACACACTATCCAACTTAATATGATCAT 939
DB 787 ATTGCTGACACAGTCCAGTTCAGGACCTTATGACACACTATCCAACTTAATATGATCAT 846
QY 940 TTAAATTCAGTAAAGTGATCACTTTCAGAAATCTGATTTCCCTATTTTACCACTGCACA 999
DB 847 TTAATATCAGCAAGTGATCACTTTCAGAAATCTGATTTCCCTATTTTACCACTGCACA 906
QY 1040 GTGAATCCAAAGAAAGTATAGTCAAAAGAGTGAAGCATATAGCATACATCTTTTAAAGAG 1059
DB 907 GTGAATCCAAAGAAAGTATAGTCAAAAGAGTGAAGCATATAGCATACATCTTTTAAAGAG 966
QY 1360 AAAATTCATAGGCTGAGGACACAGGCTGAGTGGAAATGATGATACAGAGGATACAACTT 1119
DB 947 AAAATTCATAGGCTGAGGACACAGGCTGAGTGGAAATGATGATACAGAGGATACAACTT 1026
QY 1320 GCAATTCCTTATTAATGCAAGTAAATGCAATGATGCTTAAATGCAAGGAAAGCAATTA 1179
DB 1027 GCAATTCCTTATTAATGCAAGTAAATGCAATGATGCTTAAATGCAAGGAAAGCAATTA 1086
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DB 1147 GCGGCTGCTTGAGGCTGCTTAAAGGACACATATAGGCAAGTACATCTCAGAACTGATCT 1206
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DB 1207 GCAATTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1266
QY 1360 TACAAGTGAATGGAAGTTTATGCAAGGACAGAGGCACTGTCAGACAGAAATGATTAATA 1419
DB 1247 TACAAGTGAATGGAAGTTTATGCAAGGACAGAGGCACTGTCAGACAGAAATGATTAATA 1326
QY 1420 CATTTAGAGCTGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1479
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QY 1480 TTATTTGATCTTTTAAACAACTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1539
DB 1487 TTATTTGATCTTTTAAACAACTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1446
QY 1540 GCTTGCTGCTTAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1599
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QY 1600 GCTTGCTGCTTAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1659
DB 1547 GCTTGCTGCTTAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
QY 1660 GAGATCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1719
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DB 1627 GCTTGCTGCTTAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
QY 1740 GCTTGCTGCTGAGCAGCAGAAATGAGAAATATGATGCTGAGCAGCAGCAGCAGCAGCAG 1839
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DB 1747 GAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1806

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QY 1960 AAGGATCTGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2019
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DB 2107 CTGAGGAGTCTTAT 2166
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DB 2407 AAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2466
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QY 2620 AAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2679
DB 2527 AAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2586
QY 2680 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2739
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QY 2740 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2799
DB 2647 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2706
QY 2800 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2859
DB 2707 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2766
QY 2860 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2919
DB 2767 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2826
QY 2920 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2979
DB 2827 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 2886
QY 2980 TCAAGGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTAT 3039

DB 2887 ATGAAACGCTTAGAAAATGGGCTATGCTATCATGCAATGCAATTTGATGACTGCGC 2946
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 DB 2947 AATCAACAAAATAAGCTGAAATCTCTGCGCAAAAATGCAATATATACAAATACAAAAA 3006
 QY 4100 AATCAAT 3159
 DB 4007 AATCAAT 3066
 QY 4160 TGTAT 3219
 DB 4067 TGTAT 3126
 QY 4220 TAT 4279
 DB 4127 TAT 3186
 QY 4280 TTTTTCATGCAAT 3424
 DB 4187 TTTTTCATGCAAT 3240

RESULT 4

US 08 470 091 Z/c
 3 Sequence 2, Application 05/08/170094
 3 Patent No. 5912246
 3 GENERAL INFORMATION:
 3 APPLICANT: Xu, Hong Ji
 3 APPLICANT: Hu, Shi Xue
 3 TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
 3 TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
 3 NUMBER OF SEQUENCES: 4
 3 CORRESPONDENCE ADDRESS:
 3 ADDRESSEE: Perrine & Edmunds
 3 STREET: 1155 Avenue of the Americas
 3 CITY: New York
 3 STATE: New York
 3 COUNTRY: U.S.A.
 3 ZIP: 10036, 2711
 3 COMPUTER READABLE FORM:
 3 MEDIUM TYPE: Floppy disk
 3 COMPUTER: IBM PC compatible
 3 OPERATING SYSTEM: PC DOS/MS-DOS
 3 SOFTWARE: Patent In Release #1.0, Version #1.25
 3 CURRENT APPLICATION DATA:
 3 APPLICATION NUMBER: US/08/470,091
 3 FILING DATE: JUN-16-1995
 3 CLASSIFICATION: 514
 3 PRIOR APPLICATION DATA:
 3 APPLICATION NUMBER: US/08/004,760
 3 FILING DATE:
 3 ATTORNEY/AGENT INFORMATION:
 3 NAME: Poissant, Brian M
 3 REGISTRATION NUMBER: 28,442
 3 REFERENCE/BOOK NUMBER: 7409-025-999
 3 TELECOMMUNICATION INFORMATION:
 3 TELEPHONE: (212) 790-9090
 3 TELEFAX: (212) 860-9741/8864
 3 TELEX: 66141 PENNIE
 3 INFORMATION FOR SEQ ID NO: 2:
 3 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 3242 base pairs
 3 TYPE: nucleic acid
 3 STRANDEDNESS: double
 3 TOPOLOGY: not relevant
 3 Molecule TYPE: UNA

Query Match 97.0% Score 3222.4 DB 2 Length 3242
 Best local similarity 100.0% Pred No 0;

	Matches 3243	Conservative	0	Mismatches	1	Indels	0	Gaps	0
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QY	160	CATAAATGTTTAACTTACTTAAAGAAATATGATATACATATCAAAATGATATATGCTATG	219						
DB	3170	CATAAATGTTTAACTTACTTAAAGAAATATGATATACATATCAAAATGATATATGCTATG	4111						
QY	220	TCAACACCTGTTGCAATAGATGATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	279						
DB	3110	TCAACACCTGTTGCAATAGATGATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4041						
QY	280	TGTGAATCTATATATGACACAAATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	339						
DB	3050	TGTGAATCTATATATGACACAAATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2991						
QY	340	TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	399						
DB	2990	TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2941						
QY	400	GAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	459						
DB	2930	GAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2871						
QY	460	CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	519						
DB	2870	CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2811						
QY	520	TCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	579						
DB	2810	TCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2751						
QY	580	AATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	639						
DB	2750	AATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2691						
QY	640	AAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	699						
DB	2690	AAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2641						
QY	700	ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	759						
DB	2630	ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2571						
QY	760	AAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	819						
DB	2570	AAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2511						
QY	820	GACAGTTTGAACACACAGAC	879						
DB	2510	GACAGTTTGAACACACAGAC	2451						
QY	880	ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	939						
DB	2450	ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2391						
QY	940	TAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	999						
DB	2390	TAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2441						
QY	1000	GTCAGTTTGAACACACAGAC	1059						
DB	2330	GTCAGTTTGAACACACAGAC	2271						
QY	1060	AAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1119						
DB	2270	AAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2211						
QY	1120	GAAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1179						
DB	2210	GAAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2151						

RESULT 5
 HUS 08 204 429 2
 Sequence 2: Affiliation: US/08/204 429
 Patent No. 5710255

GENERAL INFORMATION:
 APPLICANT: SHEPARD, H. M.
 APPLICANT: WEN, SHU F.
 TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
 TITLE OF INVENTION: MONOCLONAL ANTIBODY
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
 STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: U.S.A.
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: pc-dos/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.40
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/204, 429
 FILING DATE: 15 AUG 1994

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05866
 FILING DATE: 14 JUL 1992

ATTORNEY/AGENT INFORMATION:
 NAME: RENE A. FITTS
 REGISTRATION NUMBER: 45,146
 REFERENCE/DOCKET NUMBER: 16940-00040005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 426-2400
 TELEFAX: (415) 426-2422
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2974 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPLOGY: linear
 MOLECULE TYPE: DNA (cDNA)

HUS 08 204 429 2

Query Match 74.9% Score 2524; DB 1; Length 2994;
 Best Local Similarity 100.0% Prod. No. 0;
 Matches 2623; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGAAGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAGGAACT 68
 DB 472 GAGAGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAGGAACT 431
 QY 69 GTGGGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAGGAACT 128
 DB 432 GTGGGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAGGAACT 491
 QY 129 GCAATATAGAAAGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAT 188
 DB 492 GCAATATAGAAAGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAT 551
 QY 189 GCAATATAGAAAGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAT 248
 DB 552 GCAATATAGAAAGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAT 611
 QY 249 GTTGTAGCTGCTGGATGAGTATGGAGGTATATTCAGAAAGAAATTCAGAAAGAAAT 308
 DB 612 GTTGTAGCTGCTGGATGAGTATGGAGGTATATTCAGAAAGAAATTCAGAAAGAAAT 671
 QY 309 GCAATATAGAAAGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAT 368
 DB 672 GCAATATAGAAAGAAATTCATGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAT 731

QY 369 TTATATAGCTAAAGAGAGGAAATTAACAAATGAGAAAGATGATGATATTCATTCAGT 428
 DB 732 TTATATAGCTAAAGAGAGGAAATTAACAAATGAGAAAGATGATGATATTCATTCAGT 791
 QY 429 AATGCTATGCTGCTGGATGAGTATGGAGGTATATTCAGAAAGAAAGGAAATTCAGT 488
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 QY 909 TATGCAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 968
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RESULT 9

PCT US94 10457 1

Sequence 1, Application PCT/US9410457

GENERAL INFORMATION:

1 APPLICANT: The Regents of the University of California
2 APPLICANT: and Calif, Inc.
3 TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
4 TITLE OF INVENTION: Susceptibility Gene Product
5 NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

1 ADDRESSEE: Campbell and Flores
2 STREET: 4470 La Jolla Village Drive
3 CITY: San Diego
4 STATE: California
5 COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC DOS/MS DOS
4 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

1 APPLICATION NUMBER: PCT/US94/10457
2 FILING DATE: 13 SEP 1994

CLASSIFICATION:

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: US 09/121,108

FILING DATE: 13 SEP 1994

ATTORNEY/AGENT INFORMATION:

1 NAME: Campbell, Cathryn A.
2 REGISTRATION NUMBER: 31,815
3 REFERENCE/DOCKET NUMBER: PP-09 1117
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (619) 545-9001
6 TELEFAX: (619) 545-8949

INFORMATION FOR SEQ ID NO:

1 1
2 SEQUENCE CHARACTERISTICS:
3 LENGTH: 2994 base pairs
4 TYPE: nucleic acid

1 STRANDEDNESS: Single
2 TOPOLOGY: Linear
3 FEATURE:
4 NAME/KEY: CDS
5 LOCATION: 149..2923
6 PCT-US94-10457 1

Query Match

Best Local Similarity 78.9%; Score 2621.4; DB % Length 2994;

Matches 2622; Conservatve 0; Mismatches 1; Indels 0; Gaps 0;

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DB 372 GCAAGAAATTCATCTGAGAGAGATAGGAGATATATATATATATATATATATATATATATAT 441

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DB 432 GAGGGAATTCATCTGAGAGAGATAGGAGATATATATATATATATATATATATATATATAT 491

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DB 492 TGAAGTAT 551

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us-09-026-459a-32.rni

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2049 GCTCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2108
 2412 GCTCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2471
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 2289 ATCTCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2348
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 2349 GCTCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2408
 2712 GCTCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2771
 2409 TATCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2468
 2772 TATCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2831
 2469 GCACAACTCTGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2528
 2832 GCACAACTCTGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2891
 2529 TATCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2588
 2892 TATCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2951
 2589 TATCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2631
 2952 TATCTTCATGACAGAGCTGAAACAAATATATTTGCAGTATGCTTCCACAGGCGCCCTAC 2994

! RESULT 10
 US-08-959-638-7
 ; Sequence 7, Application US/08959638
 ; Patent No. 5932210
 ; GENERAL INFORMATION:
 ; APPLICANT: Gregory, Richard J.
 ; APPLICANT: Willis, Ken N.
 ; APPLICANT: Mancini, Daniel C.
 ; TITLE OF INVENTION: Recombinant Adenoviral Vector and
 ; TITLE OF INVENTION: Methods of Use
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/959,638
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/38/328,573
 ; FILING DATE: 25-OCT-1994
 ; APPLICATION NUMBER: US 08/233,777

1 FILLING DATE: 19 MAY 1994
 2 PROB APPLICATION DATA:
 3 APPLICATION NUMBER: US 09/142,669
 4 FILLING DATE: 25 OCT 1995
 5 ATTORNEY/AGENT INFORMATION:
 6 NAME: Campbell, Cathryn A.
 7 REGISTRATION NUMBER: 31,815
 8 REFERENCE/PROCKET NUMBER: P CJ 1192
 9 TELECOMMUNICATION INFORMATION:
 10 TELEPHONE: (619) 545-9001
 11 TELEFAX: (619) 545-8949
 12 INFORMATION FOR SEQ ID NO. 7:
 13 SEQUENCE CHARACTERISTICS:
 14 LENGTH: 2995 base pairs
 15 TYPE: nucleic acid
 16 STRANDEDNESS: single
 17 Topology: linear
 18 FEATURE:
 19 NAME/KEY: CDS
 20 LOCATION: 139..2922
 21 DB OR 959 648 7

Query Match: 79.8%; Score 2620; Db 2; Length 2995;
 Best Local Similarity 100.0%; Prod No. 0;
 Matches 2620; Conservat 1.0; Mismatches 0; Indels 0; Gaps 0;

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 9 249 GTTGTATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 308
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 23 669 TTTATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 728
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 1932 TAATCAACATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1991
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 1689 CCAGCAAGGCAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1748
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 1749 CTATTCGCTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1808
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QY 1869 GATATTTGGACCAAAATATGATGCTGTTCCATGATGATGATGATGATGATGATGAT 1928
DB 2232 GATATTTGGACCAAAATATGATGCTGTTCCATGATGATGATGATGATGATGATGATGAT 2291
QY 1929 GATATTTGGACCAAAATATGATGCTGTTCCATGATGATGATGATGATGATGATGATGAT 1988
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DB 2952 GATATTTGGACCAAAATATGATGCTGTTCCATGATGATGATGATGATGATGATGATGAT 2991
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RESULTS:

US 09-026-459a-32

Sequence 7, Application: 05/09/2003

Patent No. 6210939

GENERAL INFORMATION:

APPLICANT: Gregory, Richard J.

Maneuval, Daniel C.

TITLE OF INVENTION: Recombinant Adenoviral Vector and

Methods of Use

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

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QY 9 GCATCAAACTTTTCACTTGGAGAGAGATATGGAGGGAATATCAAAAGAGAGAGAGAGAG 68
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COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/026-459a
FILING DATE: 25-Oct-1994
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25-Oct-1993
APPLICATION NUMBER: US 08/233,669
FILING DATE: 26-Apr-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy S.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 016930-00092005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2995 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 139..2925
OTHER INFORMATION: /product= "RB"
/note= "retinoblastoma tumor suppressor"
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-026-459a-32

Query Match

Best Local Similarity 78.8%; Score 2618.4; DB 4; Length 2995;

Matches 2619; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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1  RESULT 12
2  US 07/108-962-1
3  Sequence 1: Application US-07-08962-1
4  Patent No. 5262421
5  GENERAL INFORMATION:
6  APPLICANT: Livingston, David M.
7  APPLICANT: Ewen, Mark E.
8  TITLE OF INVENTION: Tumor Suppressor
9  NUMBER OF SEQUENCES: 1
10 ADDRESS-SEQUENCE ADDRESS: 1
11 ADDRESS-SEQ: Charles Hall & Stewart
12 STREET: Exchange Place, 53 State Street
13 CITY: Boston
14 STATE: Massachusetts
15 COUNTRY: U.S.A.
16 ZIP: 02104
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patent In Release #1 0, Version #1 25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US97/108-962
24 FILING DATE: 19910531
25 CLASSIFICATION: 435
26 ALL KEY/AGENT INFORMATION:
27 NAME: Kennedy, Bill
28 REGISTRATION NUMBER: 43,407
29 REFERENCE/POCKET NUMBER: DECI 209
30 INFORMATION INFORMATION:
31 TELEPHONE: (617) 227-5030
32 TELEFAX: (617) 227-7566
33 TELEX: 280374
34 INFORMATION FOR SEQ ID NO: 1:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 2808 base pairs
37 TYPE: NUCLEIC ACID
38 STRANDINESS: double
39 TOPOLOGY: linear
40 MOLECULE TYPE: cDNA
41 HYDROTICAL: NO
42 ANTI-SENSE: NO
43 US 07/108-962-1

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Query Match: 2.1%; Score 68.8; DB 1; Length 2808;
Best Local Similarity 53.1%; Pred. No. 1.1e-06;
Matches 170; conservative 0; Mismatches 147; indels 2

[illegible]

116 2247 A3AGW6TGTGTGTAA 256

116 2247 A3AGAGTTTCTCTTAA 256

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1 RESULT 13
2 US-08-106-493A-1
3   : Application No. US/08/106-493A
4   : Patent No. 5457049
5   : GENERAL INFORMATION:
6   : APPLICANT: Antonio Giordano
7   : TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN PRH2,
8   : TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODING
9   : TITLE OF INVENTION: THEREFOR"
10  : NUMBER OF SEQUENCES: 4
11  : CORRESPONDENCE ADDRESS:
12  : ADDRESSEE: Temple University-of the Commonwealth
13  : ADDRESSEE: System of Higher Education
14  : STREET: 406 University Services Building
15  : CITY: Philadelphia
16  : STATE: Pennsylvania
17  : COUNTRY: U.S.A.
18  : ZIP: 19122
19  : COMPUTER READABLE FORM:
20  : MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
21  : COMPUTER: IBM PS/2
22  : OPERATING SYSTEM: MS-DOS
23  : SOFTWARE: WordPerfect 5.1
24  : CURRENT APPLICATION DATA:
25  : APPLICATION NUMBER: US/08/106,493A
26  : FILING DATE: August 12, 1993
27  : CLASSIFICATION: 435
28  : PRIOR APPLICATION DATA:
29  : APPLICATION NUMBER:
30  : FILING DATE:
31  : AGENCY/AGENT INFORMATION:
32  : NAME: Mallins, J.G.
33  : REGISTRATION NUMBER: 33,073
34  : REFERENCE/DACKET NUMBER: 6056-188
35  : TELECOMMUNICATION INFORMATION:
36  : TELEPHONE: (215) 568-8383
37  : TELEFAX: (215) 568-5549
38  : TELEX: NO. 5457049C
39  : INFORMATION FOR SEQ ID NO: 1:
40  : SEQUENCE CHARACTERISTICS:
41  : LENGTH: 3249 base pairs
42  : TYPE: nucleic acid
43  : STRANDEDNESS: Single
44  : TOPOLOGY: linear
45  : US-08-106-493A-1

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Query Match 2.18, Score 68.2, DB 1, Length 3249;
Best Local Similarity 53.08; Prod. No. 1.6e-06;

[illegible]

1991 TTTTTCCTCAG 2011

1991 TTTTTCCTCAG 2011

10 2049 AAAAAAAAAAAAAAAAAA 2869

Search completed: January 17, 2003, 18:20:35
Job time : 110.19 secs

? INFORMATION FOR SEQ ID NO: 2:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 2994 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: double
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (cDNA)
 ? US-08-204-329-2

Alignment Scores:

Source: 0 Length: 2994
 Percent Similarity: 4499.00 Matches: 873
 Best Local Similarity: 100.00% Conservatives: 0
 Query Match: 100.00% Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-026-459a-31 (1-874) x US-08-204-329-2 (1-2994)

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 DB 364 TTAACCTGGAGAAAGTTTCATCTGCTGGATGGAGTATGGAGGTTATATTCAGAGAAA 423
 QY 42 LysGluLeuTrpGlyLeuGlySerPheAlaValAspLeuMetSerPhe 61
 DB 424 AAGCAACTGGGGAAGTCTGATCTTATTCGATGAGTGGAGTATGGAGGTTATATTCAGAGAAA 423
 QY 62 ThrPheThrGluLeuGlnLysAsnLeuGlyLeuSerValHisLysPhePheAsnLeuLeu 81
 DB 484 ACTTTACTCAGCTACAGAAACATACAAATCAGTGTCCATAAAATCTTTAACTTACTA 543
 QY 82 LysGluLeuAspPheSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 101
 DB 544 AAGCAAAATGATACAGTACCAAGTGTATGATGATGATGATGATGATGATGATGATGATGAT 603
 QY 102 AspValLeuPheAlaLeuGlySerLysLeuGluArgThrCysGluLeuLeuLeuLeuLeu 121
 DB 604 GAT 663
 QY 122 GluPheSerSerLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 141
 DB 664 CAACCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
 QY 142 ThrPhePheLeuAlaLysGlyGluValLeuGlnMetGluAspLeuValLeuSer 161
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 QY 162 PheGlnLeuMetLeuGlyValLeuAspTyrPheLeuLysLeuSerProMetLeuLeu 181
 DB 784 TTTGATTAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 QY 182 LysGluProTyrLysThrAlaValLeuProLeuAsnGlySerProArgThrProArgArg 201
 DB 844 AAACAACCAATATAAACAACCTGCTATACCAATATAAACAACCTGCTGCTGCTGCTGCTGCTGCT 903
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 QY 222 ValLeuGlyLysGlnHisGlyCysAsnLeuGluValLysAsnValTyrPheLysAsn 241
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 DB 2104 CGGCTAGCTCTATCTCCGCTAAATACACTTTGTCAAGCCCTTCTCTCTCTCTCTCTCTCT 2163
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QY 222 ValLeuCysLysGlnHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsn 241
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QY 242 PheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValIle 261
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QY 262 AsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeu 281
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Db 384 CTGAAAGAGCTCAAGCATATAGATACATCTTTAAAGAGAAATTTGCTTAAAGCTTGCGA 1443
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QY 542 LeuGlnAsnAsnHisThrAlaIleAspMetTyrLeuSerProValArgSerProLysLys 561
Db 564 CTCCAGAAATATACACTGACAGCAATATGATATCTTCTTCTTCTTCTTCTTCTTCTTCT 1983
QY 562 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581

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QY 602 ArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGlu 621
Db 2104 CGGCTAGCTATCTCCGCTAAATACACTTTGCAACGCTTCTGTCGAGCAGCCAGAA 2163
QY 622 LeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMet 641
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QY 642 ArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLys 661
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QY 662 AsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaVal 681
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QY 702 TyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArg 721
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RESULT 3

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US-08-001-092-3
: Sequence 3, Application US/08801092
: Patent No. 6074850
: GENERAL INFORMATION:
: APPLICANT: Antelman, Douglas
: APPLICANT: Gregory, Richard J.
: APPLICANT: Wills, Kenneth N.
: TITLE OF INVENTION: Tissue Specific Expression of
: Retinoblastoma Protein

```

1 NUMBER OF SEQUENCES: 46
 2 CORRESPONDENCE ADDRESS:
 3 ADDRESSSEE: TOWNSEND and TOWNSEND and CREW LLP
 4 STREET: Two Embarcadero Center, 8th Floor
 5 CITY: San Francisco
 6 STATE: CA
 7 COUNTRY: USA
 8 ZIP: 94111
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: Floppy disk
 11 COMPILED: IBM PC compatible
 12 OPERATING SYSTEM: PC-DOS/MS-DOS
 13 SOFTWARE: Patent In Release #1.0, Version #1.40
 14 CURRENT APPLICATION DATA:
 15 APPLICATION NUMBER: US/09/801,092
 16 FILING DATE: 14-FEB-1997
 17 CLASSIFICATION: 514
 18 PRIOR APPLICATION DATA:
 19 APPLICATION NUMBER: US 08/761,517
 20 FILING DATE: 15 NOV 1996
 21 CLASSIFICATION: 514
 22 ATTORNEY/AGENT INFORMATION:
 23 NAME: FITTS, RENE A.
 24 REGISTRATION NUMBER: 45,146
 25 REFERENCE/BOOKLET NUMBER: 016930-001020
 26 TELECOMMUNICATION INFORMATION:
 27 TELEPHONE: 415, 576-0200
 28 TELEFAX: 703, 576-0400
 29 INFORMATION FOR SEQ ID NO: 3:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 2994 base pairs
 32 TYPE: nucleic acid
 33 STRANDEDNESS: single
 34 TOPOLOGY: linear
 35 MOLECULE TYPE: cDNA
 36 US 08 801 092 3

Alignment Scores:
 Pred. No.: 0 Length: 2994
 Score: 4499.00 Matches: 873
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.89% Indels: 0
 Gaps: 0

US-09-026-459A-31 (1-874) x US 08 801-092-3 (1-2994)

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 41 42 LysGluLeuThrGlyIleCysIlePheIleAlaValAspLeuAspGluMetSerPhe 61
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 44 484 ACTTTTACTGAGCTACAGAAAATAGAAAATCAGGTGTCATATAATTCCTTAATCTACTA 543
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 1624 GTCACATATAGCAGACAGTATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCA 1683
 462 TrpIleLeuAsnValLeuAsnLeuLysAlaPheAspIleTyrLysValIleIleLeuSerPhe 481
 1684 TCGATCTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1743
 482 IleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisIleGluGluArgGlyLysHis 501
 1744 ATCAAGACAGAGCAACTTGACAGAGAGAAATGATATAAAATATTGAAATGATGAAATCAT 1803

502 AcdlleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuLeuLeuLysGln 521
 1804 CCAATCATGCAATCCCTTCATGCGTCACAGATCACTTTATTGTGATCTATTAAACAA 1863
 522 SerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuPro 541
 1864 TCAAGAGCCAG 1923
 542 LeuGlnAsnAsnHisThrAlaAspMetTyrLeuSerProValArgSerProLysLys 561
 1924 GTCCAGATAATACACTGCAGAGATATGATCTTTCTCTCTGTAAGATCTCCAAAGAA 1983
 562 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581
 1984 AAAGCTTCACACTACCGCTGTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2043
 582 PheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyr 601
 2044 TTCCAGAGCCAG 2103
 602 ArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGlu 621
 2104 CGGCTAGCTATCTCGGCTAAATACACTTTCTGAGGCTCTCTCTCTCTCTCTCTCTCT 2163
 622 LeuGlnHisLeuLeuThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMet 641
 2164 TACAGACATACATCTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2223
 642 ArgAspArgHisLeuAspGlnLeuMetMetCysSerMetTyrGlyLeuCysLysValLys 661
 2224 AG 2283
 662 AsnLeuAspLeuLysPheLysLeuValThrAlaTyrLysAspLeuProHisAlaVal 681
 2284 AATATAGACTTAAATTCATTAATCATTTGTAATAGCATACAGGATCTCTCTCTCTCT 2343
 682 GlnGlnThrPheLysArgValLeuLeuLysGluGluGluTyrAspSerLeuLeuValPhe 701
 2344 CAGCAGACATCAACAGGCT 2403
 702 TyrAsnSerValPheMetGlnArdLeuLysThrAsnLeuLeuGlnTyrAlaSerThrArg 721
 2404 TATATCTGGGCT 2463
 722 ProGlnThrLeuSerProLeuProHisLeuProArgSerProTyrLysPheProSer 741
 2464 CCGCTACTTGTACCAATACCTACATCTCTCGAAGGCTTACAAATTTCTTACTTCA 2523
 742 ProLeuArgLysProGlyLysLeuTyrLeuSerProLeuLysSerProTyrLysLeu 761
 2524 CCGTTCAGGATCT 2583
 762 SerLeuLysLeuProThrProThrLysMetThrProArgSerArgLeuValSerLeu 781
 2584 TCAAGAGCTGCTCAACACCAACAAATGACTCCAGATCAAGATCTTACTATCAATT 2643
 782 GlyLeuSerPheGlyThrSerThrLysPheGlnLysLeuAsnGlnMetValCysAsnSer 801
 2644 GGTGAATCATCTGGAGCT 2703
 802 AspArgValLeuLysArgSerAlaGluLysSerAsnProProLysProLeuLysLysLeu 821
 2704 CAGCTGCTCTCAAAAG 2763
 822 ArgPheAspLeuGluLysSerAspGluAlaAspGlySerLysHisLeuProGlyGluSer 841
 2764 CCGTTTGATTTGAGAGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2823
 842 LysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLys 861
 2824 AATATTCAGCAAAAG 2883

QY 862 MetAspSerMetAspThrSerAsnLysGluLys 874
 DB 2884 ATGAATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2922
 RESULT 4
 US-09-315-113-3
 : Sequence 3, Application us/09315113
 : Patent No 6379927
 : GENERAL INFORMATION:
 : APPLICANT: Antelman, Douglas
 : Gregory, Richard J.
 : Wills, Kenneth N.
 : TITLE OF INVENTION: Tissue Specific Expression of
 : NUMBER OF SHOWNCHES: 46
 : CORRESPONDENCE ADDRESS:
 : ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
 : STREET: Two Embarcadero Center, 8th Floor
 : CITY: San Francisco
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94111
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09315113
 : FILING DATE: 19-May-1999
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/801,092
 : FILING DATE: <Unknown>
 : AUTHORITY/AGENT INFORMATION:
 : NAME: Fitts, Renee A.
 : REGISTRATION NUMBER: 35,136
 : REFERENCE/DOC/KEY NUMBER: 216736-651020
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415-576-0200
 : TELEFAX: 703-576-0300
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2994 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 : US-09-315-113-3
 Alignment Scores:
 Prod. No.: 0 Length: 2994
 Score: 4499.00 Matches: 873
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.89% Indels: 0
 DB: 4 Gaps: 0
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 QY 2 AspPheThrAlaLeuLysCysGlnLysLeuLysLeuPheProAspHisValArgGluArgAlaTrp 21
 DB 304 GATTTACTGCTATATGTCAGAAATTAAGATACCATCATGTCACAGACAGAGCTGG 363
 QY 22 LeuThrTrpGluLysValSerSerValAspGluValLeuGlyLeuTyrLeuGluLysLys 41
 DB 364 TTAACCTGGAGAGAAAGTTTCACTGCTGATGGAGTATGGAGGTTATATTCAGAGAAA 423
 QY 42 LysGluLeuThrGlyTyrLeuCysLeuPheLeuAlaValAspLeuAspGluMetSerPhe 61
 DB 424 AAGGAACGTGGGGAATCTGTATCTTTATTCACAGCAGTTCACCTAGATGAGATGCTTC 483

QY 62 ThrPheThrGluLeuGluLysAsnIleGluIleSerValHisLysPhePheAsnLeuLeu 81
 DB 444 A*TTTAACTGAGTACAGAAAAACAATACAAAACAGCTGCCAATAAATCTAACTACTA 543
 QY 82 LysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 101
 DB 544 AAAAAGATGATACAGATATCAAGTTGATTAATGCTATGCTCAAGATGTTGGAAGAGTAT 603
 QY 102 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuThr 121
 DB 604 CAGTATATGTTGACATCTTACACAAATTCGAAAGGACATGTCGAATATATATATGACA 663
 QY 122 GluProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTyr 141
 DB 644 CAATGACACATTCGATATATGATATGAAATAAATTCGATGCTGCTGCTGCTGCTGCTG 723
 QY 142 IleThrPheLeuLeuAlaLysGlyGluValLeuGluMetGluAspPheValIleSer 161
 DB 744 ATACATTTTATTAGTTAAGGGGAAGTATTACAAATGGAAATATGATCTGGTGATTCA 783
 QY 162 PheGluLeuMetLeuGlyValLeuAspTyrPheIleLysLeuSerProProMetLeuLeu 181
 DB 784 TTTGATTAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
 QY 182 LysGluProTyrGluThrAlaValIleProIleAsnGlySerProArgThrProArgArg 201
 DB 844 AAAAAGACATATAAAACAGCTGTTTACCCATTAATGGTTCATCTGCAACACCCAGCCCA 903
 QY 202 GlyGluAsnArgSerAlaArgIleAlaLysGluLeuGluAsnAspThrArgIleLeuGlu 221
 DB 904 GGTACAGACAGATGTCAGGATAGTAAACACTAGAAATATATACAGCAATTATTGAA 963
 QY 222 ValLeuLysLysGluHisGlyCysAsnIleAspGluValLysAsnValTyrPheLysAsn 241
 DB 964 GTCCTGCTGAAGAACATGAATGATTAATACATCAGCTGCAAGCTGCAAGCTGCAAGCT 1023
 QY 242 PheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGlu 261
 DB 1024 TTTAATCTTTTATCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
 QY 262 AsnLeuSerLysArgTyrGluGluIleTyrLeuLysAspLeuAspAlaArgLeu 281
 DB 1084 AAATTTTCAAAACATAGAAAGAAATTTATCTTAAAAATTAAGATATAGATGCAAGATTA 1143
 QY 282 PheLeuAspHisAspLysThrLeuGluIleThrAspSerIleAspSerPheGluThrGlnArg 301
 DB 1144 TTTTGGATATGATGATAAAACCTTCAGACTGATCTATAGACAATTTTCAAAACACACAGA 1203
 QY 402 ThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVal 321
 DB 1204 ACAACAGAAAGGAAAGCTTGAAGAGAGTCAATGCTAATCTCCACACACTCCAGTT 1263
 QY 422 ArgThrValMetAsnThrIleGluGluLeuMetMetIleLeuAsnSerAlaSerAspGln 341
 DB 1264 AGGATGCTTATGAAACATATGCAACCAATTAATGATGATTTAAATTCACCAAGTGATCAA 1323
 QY 442 ProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIle 361
 DB 1324 CTTCTCAAAAAACATCTCTCTATTTTAAACACCTGACAGTGAATCCAAAGAAAGATA 1383
 QY 662 LeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGly 381
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 QY 882 GluGlyLysValGluIleGlySerGluArgTyrLysLeuGlyValArgLeuTyrTyrArg 401
 DB 1444 CAGATGCTGTGTGAAATGGATACAGAGGATAGAAATCTGGAGTCTGCTGCTGCTGCTGCTG 1503
 QY 402 ValMetGluSerMetLeuLysSerGluGluArgLeuSerIleGluAsnPheSerLys 421
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DB 1564 CTTCTGAATGACAAACATTTTTCATATGCTTTATTTGGTGGTCTCTTGAGTTGATTC 1623
 QY 442 AlaThrTyrSerArgSerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPhePro 463
 DB 1624 GCCCATATAGCAGAGATGATCTCAGATCTTGATTTGAAACAGATTGTTTTCGCA 1683
 QY 462 TrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPhe 481
 DB 1684 TGGATCTCGAATGCTCTAAATTAAGAGCTTTCATTTTACAAAGCTGACGCAAACTTT 1743
 QY 482 IleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHis 501
 DB 1744 ATCAAGSCAGAGGCAATTCGAAAGAGAAATGATAAANAATTTAAAGATGTAAT 1803
 QY 502 ArgIleMetGluSerLeuAlaIlePheLeuSerAspSerProLeuPheAspLeuIleCysHis 521
 DB 1804 GGAATCATGGAATCCCTTGCATGGCTCTCAGATTCAGTTTATTTATTTATTAANA 1863
 QY 522 SerLysAspArgGluGlyProThrAspHisIleLeuLeuSerAlaCysProLeuAsnLeuPro 541
 DB 1864 TCAAGGACCCACAAAGCAACCAACATGATCAGCTTCAATTCGCTGCTGCTGCTGCTGCT 1923
 QY 542 LeuGluAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValAlaSerProLysLys 561
 DB 1924 CTCAGAAATATACATGAGAGAGATATGATCTTCTGCTGTAATATCTGCAAGAAA 1983
 QY 562 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAla 581
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 QY 582 PheGluThrGluLysProLeuLysSerThrSerLeuSerLeuPheTyrLysValTyr 601
 DB 2044 TCCAGACCCCAAGAACCAATTCAAATCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2103
 QY 602 ArgLeuAlaTyrLeuArgLeuAsnThrLeuLysSerLeuLeuLeuSerGluHisProGlu 621
 DB 2104 GGGTAGCTATCTGGAGCAAAATACCTTGTCAAGCTCTGCTGCTGCTGCTGCTGCTGCT 2163
 QY 622 LeuGluHisIleIleThrThrLeuPheGluHisThrLeuGluAsnGluTyrGluLeuMet 641
 DB 2164 TTAGAAATATGATCTGCTGCTGCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2223
 QY 642 ArgAspArgHisLeuAspGluIleMetMetCysSerMetTyrGlyIleCysLysValLys 661
 DB 2224 AGACACGCTATTTGCAATTCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2283
 QY 662 AsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaVal 681
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 QY 682 GlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValPhe 701
 DB 2344 CAGAGACATTCGAAATGCTTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2403
 QY 702 TyrAsnSerValPheMetGluArgLeuLysThrAsnIleLeuGluIleThrAlaSerThrArg 721
 DB 2404 TATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2463
 QY 722 ProThrThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSerSer 741
 DB 2464 CCGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2523
 QY 742 ProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProLysLysIle 761
 DB 2524 CCGCTAGGATTCCTGAGGGAATATATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2583
 QY 762 SerGluGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIle 781
 DB 2584 TCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2643
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2644 GUTTAATGATTCGGACTTCAGAAAGTTCCAGAAATAAATCAGATGGTATTAACAGC 2703
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RESULT 5

US-08 959-638-7
 : Sequence 7, Application US/08959638
 : Patent No. 5932210
 : GENERAL INFORMATION:
 : APPLICANT: Gregory, Richard J.
 : APPLICANT: Willis, Ken N.
 : TITLE OF INVENTION: Recombinant Adenoviral Vector and
 : TITLE OF INVENTION: Methods of Use
 : NUMBER OF SEQUENCES: 9
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Campbell and Flores
 : STREET: 4370 La Jolla Village Drive, Suite 700
 : CITY: San Diego
 : STATE: California
 : COUNTRY: USA
 : ZIP: 92122
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/959,638
 : FILING DATE:
 : CLASSIFICATION:

PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/08/328,673
 : FILING DATE: 25-OCT-1994
 : APPLICATION NUMBER: US/08/233,777
 : FILING DATE: 19-MAY 1994
 PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/142 664
 : FILING DATE: 25-OCT-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Campbell, Cathryn A.
 : REGISTRATION NUMBER: 31,RL5
 : REFERENCE/DOCKET NUMBER: P-CJ 1192
 : TELEPHONE: (619) 535-9001
 : TELEFAX: (619) 535-8949
 : INFORMATION FOR SEQ ID NO: 7:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2995 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: Linear
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 139..2922
 : US-08-959-638-7

Alignment Scores: 0 Length: 2995
 Pred. No.:

Score: 4499.00 Matches: 873
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.89% Indels: 0
 DB: 2 Caps: 0
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 QY 2 AspPheThrAlaLeuGlyCysGlnLysLysLysLysLysLysLysLysLysLysLysLys 21
 DB 304 CATTTTACTGCATTATGTCAGAAATTAAGCATACCCAGATCATGTCACAGAGAGAGTTCG 363
 QY 22 LeuThiTrpGlnLysValSerSerValAspGlyValLeuGlyLysLysLysLysLys 41
 DB 364 TTAACTTGGGAGAAAGTTTCACTGTCGATGGAGTATTCGGAGGTTATATCAAAAGAAA 423
 QY 42 LysGluLeuTrpGlyLysCysLysPheLysAlaAlaValAspLeuAspGluMetSerPhe 61
 DB 424 AAGCAACTGTGGGAATCTGTATCTTTATTTGACGAGTTCAGCTAGATGAGATGCTGTTG 483
 QY 62 ThrPheThrGlnLeuGlnLysAsnLysGluLysSerValHisLysPhePheAsnLeuLeu 81
 DB 484 ACTTTTACTCAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATCTCTTAACITACIA 543
 QY 82 LysGluLeuAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 101
 DB 544 AAAGAAATTCATACCCAGTACCAAGTTGATAATGCTATCTCAAGACTGTTCAACAAGTA 603
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 DB 784 TTTGATTAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 QY 182 LysGluProTyrLysThrAlaValLysProLysGlySerProArgThrProArgTyr 201
 DB 844 AAACAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTGCAACACACAGGCA 903
 QY 202 GlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgLysLysLys 221
 DB 904 GCTTGAAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
 QY 222 ValLeuCysLysGluHisGluCysAsnLysAspGluValLysAsnValTyrPheLysAsn 241
 DB 964 GTTCTCTGTAAAGAACATGAATGTAATAGATGATGATGATGATGATGATGATGATGATGAT 1023
 QY 242 PheLysProPheMetAsnSerLysGlyLeuValThrSerAsnGlyLeuProGluValGlu 261
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 DB 1084 AATCTTTCTTAACGATACCAAGAAATTTTATCTTAATAATTAACATCTAGATGTAAGATA 1143
 QY 282 PheLeuAspHisAspLysThrLeuGlnThrAspSerLysLysLysLysLysLysLysLys 301
 DB 1144 TTTTGGATCATGATAAAACTCTTACAGCTGATCTATAGACAGTTTGTAAACACAGAGA 1203
 QY 302 ThrProArgLysSerAsnLeuAspGluGluValAsnValLysProPheLysThrProVal 321
 DB 1204 ACACACGAAAAAGTAACTGATCAACAGGTCAGTGAATGTAATCTGCTGCTGCTGCTGCTGCT 1263
 QY 322 ArgThrValMetAsnThrLysGlnGlnLeuMetMetLysLeuAsnSerAlaSerAspGln 341

1 INFORMATION FOR SEQ ID NO: 1:

2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 2994 base pairs
 4 TYPE: nucleic acid
 5 STRANDEDNESS: single
 6 TOPOLOGY: linear
 7 FEATURE:
 8 NAME/KEY: CDS
 9 LOCATION: 139..2923
 10 ECT US94-10357-1

Alignment Scores:

11 Pred. No.: 0 Length: 2994
 12 Score: 4496.00 Matches: 872
 13 Percent Similarity: 100.00%
 14 Best Local Similarity: 1
 15 Query Match: 99.89%
 16 Indels: 0
 17 Gaps: 5

18 US-09-026-459a-31 (1-874) x rni-US94-10357-1 (1-2994)

QY 2 AspPheThrAlaGlyGlyGlnLeuLysIlePheAspHisValArgAlaTrp 21
 ID 304 GATTTTACTGCTATATCTCAGAAATTAACATACAGAGTCACTGTCACACACACACTTGG 363
 QY 22 LeuThrTrpGlnLysValSerSerValAspGlyValLeuGlyGlyTrpIleGlnLys 41
 ID 664 TTAACCTGGGAGAAAGTTTATCTGTGGATGGAGTATGGAGGTATATTCAAAGAAA 423
 QY 42 LysGlnLeuTrpGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 43
 ID 424 AAGCAACTGGGCAATCTGATCTTATTTATTCACAGCTTGACCTAGAGATGCGTTC 483
 QY 62 ThrPheThrGlnLeuGlnLysAsnIleGlnLysValHisLysPheAsnLeuLeu 81
 ID 494 ACTTTTACTGAGCTACAAAGAAACAGAAATCACTGTGCAATAAACTTAACTTAACT 543
 QY 82 LysGlnIleAspThrSerThrLysValAspAsnAlaMetSerArgIleLeuLysLys 101
 ID 544 AAAAATATGATACAGTACCAAGTGTATATGCTATATGATATGATATGATATGATAT 603
 QY 102 AsnValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 121
 ID 604 GATGATATGTTTGGCACTCTTCAGCAAAATGCAAGGACATCTCAACTTATATATTTC 663
 QY 122 GlnProSerSerIleSerThrGlnLeuAsnSerAlaLeuValLeuLysValSerTrp 141
 ID 664 CAACCAACAGTTCGATACATACATCAAAATTAATTTGCTTAAAGTTTCTTGG 723
 QY 142 ThrThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 161
 ID 724 ATCAATTTTATTAGCTAAGGAGAAATATATATATATATATATATATATATATAT 783
 QY 162 PheGlnLeuMetLeuGlyValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 181
 ID 784 TTTACATTAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 QY 182 LysGlnProTrpLysThrAlaValIlePheLysAsnLysSerProArgThrProArg 201
 ID 844 AAACCAACATATAAAGACGCTTATACCATTTAATGGTTCACCTCCAAACCAACGCG 903
 QY 202 GlyGlnAsnArgSerAlaArgGlnAlaLysGlnLeuGlnAsnAspThrArgIleLeu 221
 ID 904 GGTAGAACAGGAGTGCAGAGATAGCAAAACACTAGAAATATATATATATATAT 963
 QY 222 ValLeuLysLysGlnHisLysCysAsnIleAspGlnValLysAsnValTrpPheLys 241
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 QY 242 PheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGlnVal 261
 ID 1024 TTTAAGCTTTTAAAGTATCTTGGACCTTGTAACTATTAACATCTAATGGACTTCC 1083

QY 262 AsnLeuSerLysArgTrpGluGluIleTrpLeuLysAsnLysAspLeuAspAlaArgLeu 281
 ID 1084 AATCTTTTAAAGGATACGAGAAATTTATCTTAAAAATAAAGATGATGATGCAAAATTA 1143
 QY 282 PheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArg 301
 ID 1144 TTTTGGATCATGAAAAACTCTTCACACATGATCTATACACAGTTTTCAGAACACAGACA 1203
 QY 302 ThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVal 321
 ID 1204 ACACCAAGAAAAAGTAACTTTGATGAAGAGTGAATGTATTTCTCCACACACTTCAGTT 1263
 QY 322 ArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGln 341
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 QY 362 LeuLysArgValLysAspIleGlyTrpIlePheLysGlnLysPheAlaLysAlaValLys 381
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 QY 382 GlnGlyCysValGlnIleGlySerGlnArgTrpLysGlnGlyValArgLeuTrpLysArg 401
 ID 1444 CAGGTTGTGTGAAATTTGATCTATATATGATATGATATGATATGATATGATATGAT 1503
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 QY 422 LeuLeuAsnAspAsnIlePheHisMetSerLeuLeuLysAlaLeuGluValValMet 441
 ID 1564 TTTTCTAATGACACACTTTTCAATGCTTTTATGAGTGTGAGTCTTGTGAGTGTGATG 1623
 QY 442 AlaThrTrpSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPhePro 461
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 ID 1684 TGGATCTGCAATGCTTAAATTTAAAGCTTTGATTTTACAAAGTATCGAAAGTTTT 1743
 QY 482 IleLysAlaGlnGlyValAsnLeuThrArgGluMetIleLysHisLeuGlnArgLysHis 501
 ID 1744 ATCAAGACAGAGGACACTTGCAGAGAGAAATGATAAACATTTAGAGAGATGATGAAAT 1803
 QY 502 ArgIleMetGlnSerIleAlaTrpLeuSerAspSerProLeuPheAspLeuLysGln 521
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 QY 562 LysGlySerThrThrArgValAsnSerThrAlaAsnValGlnThrClnAlaThrSerAla 581
 ID 1984 AAAGTCTCAACTACGCTGCTTAAATCTACTGCATATGACAGACACAGCAACATCAAGCT 2043
 QY 582 PheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTrpLysLysValTrp 601
 ID 2044 TTCCACACCCAGAGCCATGAAATCTACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2103
 QY 602 ArgLeuAlaTrpLeuArgLeuAsnThrLeuGlyGlnArgLeuLeuSerGlnHisProGln 621
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[illegible]

US 08 048 760 1

September 1, Application US/08048760

Patent No. 5496781

GENERAL INFORMATION:

APPLICANT: Xu, Hong Ji

APPLICANT: Xu, Shi Xue

APPLICANT: Benedict, William F.

TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and

METHODS for Tumor Suppressor Gene Therapy.

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/048 760

FILING DATE: 1999/02/25

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 7409 025-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790 9090

TELEFAX: (212) 869 9741/8864

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3212 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: not relevant

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 19...2469

US 08 048 760 1

Alignment Scores:

Prod. No.: 0

Score: 4214.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Matches: 94.94%

Gaps: 1

US 09 026 459a 31 (1 874) x US 08 048 760 1 (1-3242)

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DB 247 TTGGTGGTAAAAAGTTTCCTGGATTCACATTTTATATTAAGGCGGAAATATATCAAAATG 406
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 DB 307 GAACATGATCTGGTGATTTTCATTTTCAGTTAATGCTATGCTGCTTCACTATATTTAAAA 466
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 Q7 195 SerProArgThrProArgArgGlyGluAsnArgSerAlaArgLleAlaLysGluLeuGlu 214
 DB 427 TCACCTCCACACCCAGCGGACAGACAGAGTCCAGAGTCCAGGATCCAGGATCCAGGATCC 486
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 Q7 415 SerLleGluAsnProSerLysLeuLeuAsnAspAsnLlePheHisMetSerLeuLeuAla 434
 DB 1087 TCCATTCAAAAATTTTAGCAAACTTCTGAAATGACAAATATTTTTCATATGCTTTTATGGG 1146
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QY 555 ProValArgSerProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 574
Db 1507 ATGTAATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1566
QY 575 GluThrLeuAlaThrSerAlaPheGluThrGlnLeuProLeuLeuLeuLeuLeu 594
Db 1567 CAGACATACGACATACGACATACGACATACGACATACGACATACGACATACGAC 1626
QY 595 LeuPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 614
Db 1627 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
QY 615 LeuLeuSerGluHisProGluLeuGluHisLeuLeuLeuLeuLeuLeuLeuLeu 634
Db 1687 GTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1746
QY 645 GlnAsnGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 654
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QY 655 TyrllyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 674
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QY 675 LysAspLeuProHisAlaValGlnGluThrPheLeuArgValLeuLeuLeuLeu 694
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QY 695 TyrAspSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 714
Db 1947 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1986
QY 715 LeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 734
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RESULT 9

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US-08-038-760 2/c
: Sequence 2, Application US/08038760
: Patent No. 5496731
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: APPLICANT: Xu, Shi-Xue
: APPLICANT: Benedict, William F.
: TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
: TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/038,760
: FILING DATE: 19930325
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Polissant, Brian M
: REPRESENTATION NUMBER: 28-462
: REFERENCE/PACKET NUMBER: 7409-025-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 859-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3232 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: US-08-038-760-2
:
: Alignment Scores:
: Pred. No. 0 Length: 4232
: Score: 4213.00 Matches: 820
: Percent Similarity: 100.00% Conservative: 0
: Best Local Similarity: 100.00% Mismatches: 0
: Query Match: 93.54% Indels: 0
: DB: 1 Gaps: 0
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: QY 115 CysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluLeuAsnSerAla 134
: Db 3050 TGTGAACCTTATATTTGACACAAACCCAGCAGTTCGATATCTACGAAATAAAATCTG 2991
: QY 135 LeuValLeuLysValSerTyrPheLeuLeuAlaLysGlyGluValLeuGluMet 154
: Db 2991

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145 1487 TATTTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1446
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147 1447 GCTTGTGCTTTTAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1506
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160 615 LysAspLeuProHisAlaValGluGluThrPheGlySerValGluGluGluGluGluGluGluGlu 694
161 1867 AAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1926
162 615 TyrAspSerIleValPheTyrAsnSerValPheMetGluArgLeuLysThrAsnIle 714
163 1927 TATGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1986
164 715 LeuGlnIleValAlaSerThrArgProProThrLeuSerProIleProHisIleProArgSer 734
165 1987 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2046
166 715 ProGlyIleSerProSerProLeuArgIleProGlyIleGlyAsnIleGlyIleSerPro 754
167 2047 GTTATCAAGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2106
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180 RESULT 11
181 US-08-470-091-2/c
182 : Sequence 2, Application US/08470091
183 : Patent No. 5912236
184 : GENERAL INFORMATION:
185 : APPLICANT: Xu, Hong-Ji
186 : APPLICANT: Hu, Shi-Xue
187 : APPLICANT: Benedict, William F.
188 : TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
189 : METHOD OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
190 : NUMBER OF SEQUENCES: 3
191 : CORRESPONDENCE ADDRESS:
192 : ADDRESSEE: Pennie & Edmonds
193 : STREET: 1155 Avenue of the Americas
194 : CITY: New York
195 : STATE: New York
196 : COUNTRY: U.S.A.
197 : ZIP: 10036-2711
198 : COMPUTER READABLE FORM:
199 : MEDIUM TYPE: Floppy disk
200 : COMPUTER: IBM PC compatible
201 : OPERATING SYSTEM: PC-DOS/MS-DOS
202 : SOFTWARE: PatentIn Release #1.0, Version #1.25
203 : CURRENT APPLICATION DATA:
204 : APPLICATION NUMBER: US/08/470,091
205 : FILING DATE: JUN-16-1995
206 : CLASSIFICATION: 514
207 : PRIOR APPLICATION DATA:
208 : APPLICATION NUMBER: US/08/038,760
209 : FILING DATE:
210 : ATTORNEY/AGENT INFORMATION:
211 : NAME: Polissant, Brian M.
212 : REGISTRATION NUMBER: 28,462
213 : REFERENCE/PACKET NUMBER: 7409-025-999
214 : TELECOMMUNICATION INFORMATION:
215 : TELEPHONE: (212) 790-9090
216 : TELEFAX: (212) 869-9741/8864
217 : TELEX: 66141 PENNIE
218 : INFORMATION FOR SEQ ID NO: 2:
219 : SEQUENCE CHARACTERISTICS:
220 : LENGTH: 3232 base pairs
221 : TYPE: nucleic acid
222 : STRANDEDNESS: double
223 : TOPOLOGY: not relevant
224 : MOLECULE TYPE: DNA
225 : US-08-470-091-2
226
227 Alignment Scores:
228 Pred. No.: 0 Length: 4242
229 Score: 4213.00 Matches: 820
230 Percent Similarity: 100.00% Conservat: 0
231 Best Local Similarity: 100.00% Mismatches: 0
232 Query Match: 93.54% Indels: 0
233 Gaps: 0
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237 55 AspLeuAspGluMetSerPheThrPheGluGluGluLysAsnIleGluSerVal 74
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240 75 HisLysPhePheAspGluLeuLysGluIleValAspThrSerThrLysValAspAsnAlaMet 94
241 3170 CATAAATTCCTTAACTTACTTAAAGAAATTCATACAGTACCAACAGCTTGATAATGATG 4111
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243 95 SerArgLeuLeuGlySerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGly 114
244 3110 TCAAGATGCTGTGTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4051

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DB 445) CTTCTCCACAGGTAAGTAAAGACCGT 4477
 RESULT 14
 US 08 842 877 1
 Sequence 1: Application US/08842877
 Patent No. 5845506
 GENERAL INFORMATION:
 APPLICANT: Giordano, Antonio
 TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
 TITLE OF INVENTION: CANCER
 NUMBER OF SEQUENCES: 116
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEIDEL, GONIA, LAVAGNA & MENACCO, P.O.
 STREET: Suite 1800 Two Penn Center Plaza
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: pc Posix/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/842,877
 FILING DATE:
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Monaco, Daniel A
 REGISTRATION NUMBER: 40,480
 REFERENCE/BOOK NUMBER: 8421 14 US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568 8483
 TELEFAX: (215) 568 5549
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4853 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: cUS
 LOCATION: 70..4889
 US 08 842 877 1
 Alignment Sources:
 Prod. No.: 4360-75 Length: 4853
 Score: 775.00 Matches: 274
 Percent Similarity: 56.12% Conservat: 165
 Best Local Similarity: 23.76% Mismatches: 454
 Query Match: 17.21% Indels: 498
 Gaps: 46
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 QY 3 PheThrAlaLeuGlySerValAspGluValProAspIleValArgGluArgAlaTrpLeu 22
 DB 214 TTGAGACAGTGTGTGACGGGCTCAACATGACGAGGCGGCGGCGGAGGCGCTGGGAC 273
 QY 23 ThrTrpLeuGlyValSerValAspGlyValLeuGlyValLeuGlyValLeuGlyValLeu 42
 DB 274 AGTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 315
 QY 45 GluLeu TrpGlyIleCysIlePheIleAlaVal----- 54
 DB 416 GATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 375
 QY 55 AspLeuAspIleMetSerPheThrPheThrGluLeuGlnLeuGlnLeuGlnLeuGlnLeu 71
 DB 476 AGTAAAGGAGAGTGGAGAGGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 435
 QY 72 ThrSerValHisGlyPhePheAsnLeuLeuGlySerValLeuGlySerValLeuGlySerVal 91

DB 436 CAGACCTTAACTGAAATTTTAAATAACATGACCAACAGGAGACAAATGCGTAAATCTACCT 495
 QY 92 -----AsnAlaMetSerArgLeuLeuLeuLysLysTyrAspValLeuPheAlaLeu 107
 DB 496 CCAATTTCCACAGAAAGCTACGACAGATAGAGAAAGAACTTTACTGTTCTGCTGCTAAAT 555
 QY 108 PheSerLysLeuGluArgThrCysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 123
 DB 556 TTTAAGAAATATGAAACCATTTTTCAGGCAATCTTTTAATATGCTCAAGAGAGAGAACT 615
 QY 124 SerSerSerIleSerThrGlu-----IleAsnSerAlaLeuValLeuLys 148
 DB 616 CCTCAG 675
 QY 139 ValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuLeuMetGlnAspAspLeu 158
 DB 676 TTTTCTGGGGCTTTTTATAATAGCAAAAGCTAAATTTCTCAATGATGATGATGATGATGATG 745
 QY 159 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerProPro 178
 DB 746 GTCAATTTTATCATCTGT 777
 QY 179 MetLeuLeuLysGluProLysThrAlaValLeuProIleAsnGly----- 194
 DB 778 -----TATGCAAAATGTACTTACGTTTCAATGTTTAAATGAAAGAAATTTGCTG 819
 QY 195 SerProArgThrProLysArgGlyGluAsnArgSerAlaArgIleAlaLysGlnLeuGlu 214
 DB 820 AACCTTAATTTAAAGCTTATCAGGAATATTCATGCTAAAGATCTTAAATCTTCTCTCT 879
 QY 215 AsnAspThrArgIleGluValLeuCysLysGlnHisGlnLysAsnLeuAspIleVal 244
 DB 880 GAGCCCTTGTATCATGAGAACTGT 949
 QY 235 LysAsnVal-----TyrPheLysAsnPheIleProIleMet----- 246
 DB 940 AAGCGATATAAGCAACATTTCTGCAACCTTATATAGCAAACTTTTACAAAAAAGCTTC 949
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 DB 1000 CTAAAGCGAAAGCAAAATCTCTGCTTCTTCAACATGAGCAACTTTTACAGACAGAT 1059
 QY 269 ValGluAsnLeuSerLysArgTyrGluGluLeuLeuLysLysAsnLysAspLeuAspAla 279
 DB 1060 TTTAAGCCATCAATAAGGCTATGAGAGATGTTTATCTGTTGGGAATTTAATAGAG 1119
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 DB 1120 CCGATATTTCTTGGCAAGGATGTTGAGAGAGGAAATTTGGCACTCTCTCAAGGCTCTGCAAT 1179
 QY 287 ---LysThrLeuGlnThrAspSerIle-----AspSer----- 296
 DB 1180 GCTGGTTTCAGCAACAGACACTGTGAGAAAGCTGTGACAGACGAGAAACATCTTAAATACAT 1249
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 DB 1360 ACCATGCTGACAGGCGCTCAGGCAATGCCACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1419
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 DB 1420 TGTTCAGACATCCACCCAGGCTATGCTATACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1479
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 451 AsnLeuAspSerGlyThrAspLeuSerPheProIleLeuLeuAsnValLeuAsnLeuLys 470
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 491 GluMetIleLysIleLeuLysGlnIleValIleValIleValIleValIleValIleValIle 510
 1810 GAGTGTGTAAGACCTTTAAATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1869
 511 SerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 527
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 528 -----ProThrAspHisIleGluSerAla-----CysProLeuAsnLeuPro 541
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 542 LeuGluAsnAsnHis----- 546
 1990 TTACATCCCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2049
 547 -----ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLys 562
 2050 ACATCTGCAACACATTATAGAT 2109
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 570 Ser-----ThrAlaAsn----- 573
 2230 GATATCTGCACTTAAATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2289
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 2290 CAAAGCTATATCTTAT 2349
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 2530 CAGTGTATGCACTTAAATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2589

598 LysLysValTyrArgLeuAlaTyrIleuArgLeuAsnThrLeuCysGluArgLeu-----Leu 616
 2590 AAAAAATATAATTTAT 2649
 617 SerGluHisProGluLeuGluHisIleIleThrPheThrLeuPheGlnHisThrLeuGlnAsn 636
 2650 TCAAT-----CAATTCAGAGAAAAAATCAGACCTGCTTGAATTCGACATTAATTCAC 2703
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 2704 TCTCTGCACTTAAATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2753
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 2764 ATGTATAAAGTATAAAAAAATAAGTATTTTAAATATATATATATATATATATATAT 2823
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 3064 GAATATGAG 3123
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 3124 ACATTTGCACTGATGAGTACAGAGCAAAATATATATATATATATATATATATATATATAT 3183
 730 HisIleThrArgSerProTyrIlePheTyrProSerSerProLeuArgIle-----Pro 746
 3184 TTTGTAGAA-----ACAGCTGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 3245
 747 GlyGlyAsnIleTyrSerProLeuLysSerProTyrLysIleSerGluGlyLeuPro 766
 3226 AATCATCTCTCTACATTTCCCGCCACATAAAAAT----- 3258
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RESULT 14
 US-07-708-962-1
 : Sequence 1, Application US/07708962
 : Patent No. 5,452,321

IMMEDIATE SOURCE:

CLONE: cDNA encoding p107
US 08 152 721B-1

Alignment Scores:

Prod. No.: 2,560,74 Length: 2808
Score: 764.00 Matches: 246
Percent Similarity: 86.17% Conservative: 140
Best Local Similarity: 24.97% Mismatches: 269
Query Match: 16.94% Indels: 46
Gaps: 30

US 09 026 459A 31 (1 874) x US 08 152 721B-1 (1 2808)

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QY 110 LysLeuGluArgThrCysGlnLeuLeuThrGlnProSerSerIleSer 128
Db 64 GCAAGTTTACAGCA-----AGCGGAGAGCAGAGGAGGATTGCT 102

QY 129 ThrGluIleAsuSerAlaLeuValLeuLysValSerTyrIleThrPheLeuAlaLys 148
Db 103 TGACATTAAGCAT-----CIGCTTAATTCCTGGACATTTTGTGTATCTAAG 156

QY 149 GlyGluValLeuGlnMetGluAspLeuValIleSerPheGlnLeuMetLeuCysVal 168
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QY 169 LeuAspTyrPheIleLys-----LeuSerPro 177
Db 217 TGGATCTGATTTTGGCAATGGATTATGTGGCGAAATATACAGACATTGCTAAATGCC 276

QY 178 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAspLysSerPro 196
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QY 197 ArgThrProArgArgGlyGlnAsuArgSerAlaArgIleAlaLysGlnLeuGluAsnAsp 216
Db 437 GGTGTC----- 342

QY 217 ThrArgIleThrGluValThrCysGlnLeuIleSerAspIleValLysAsp 236
Db 443 ATCATTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 396

QY 237 Val-----TyrPheLysAsuPheIleProPheMetAsuSerLeuGlyLeuValThr 253
Db 597 ATAAAGCACTACTTAAAGCAATAATTCATAAATCTCTTACAGCAAGATATATAAA 456

QY 264 SerAsuGlyLeuProGluValGluAsu-----LeuSerLysArg 266
Db 457 GGAATATGGTCTGAGGATTTCAAGTTTATGATATATAGCAAGAGAGGAAATANGAG 516

QY 267 TyrThrGluThrCysLeuLysAspLeuAspAlaArgLeuPheLeuAspHisAsp 286
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QY 287 LysThrLeuGluThrAspSerIleAspSerPheGluThrGlnArgThrProArgLys 305
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QY 306 SerAsuLeuAspGluValValAsnVal-----IlePro 316
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QY 317 ProHis----- 318
Db 670 CAGATCTTTGAAAAAAGATGTTTGTGACCTCTTACGCTTACGCTTACGCTTACG 729

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Db 850 GAATCTTGTGTCGTAATCTGCGAAAAATATCAAAAAATATCAAAAGCAATAGAGAG 409

QY 371 IlePheLysGluLysIleAlaLysAlaValAlaLys-----GlyPheValIle 482
Db 910 ACTTCTGTCAACACATACATCAACACAGACAGAACATCAGGATCTTATACATAC 469

QY 388 GlySerGlnArgTyrLysLeuGlyValAlaPheLeuTyrArgValMetIleSerMetLeu 407
Db 970 GCTGTAATAGACTAAGCTGGCAGAAATTTTGTATTATATAAATATATAGATCTAATG 1029

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QY 448 ThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIleIleLeuAsuValLeu 467
Db 1144-----TCACCTGTACTTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1179

QY 468 AsnLeuLysAlaPheAspPheTyrLysValIleGlnLeuSerPheIleLysAlaLeuLysAsp 487
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Db 1240 CTCICAAAGGACATGCTGAAACACCTTAAACAGATGAGAAATGCTGCTGCTGCTG 1299

QY 508 AlaTTPLeuSerAspSerProLeuPheAspLeuIleLysGlnIleSerLysAspArg 525
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QY 525----- 525
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QY 525----- 525
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QY 525----- 525
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QY 525----- 525
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QY 525----- 525
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QY 526-----GluTyrProThrAspHisLeuGlnIleSerAlaLysProLeuAsp 549
Db 1720 ACAGCCCACTTAAACAGAGCAACACAGCAAT-----AAAGTAAATATATATAT 1776

QY 540-----LeuProLeuGlnAsuAsuHisThrAlaAlaAsp 550
Db 1777 GCAATATGCTGGAGAGATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1846

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561 Met Tyr Leu Ser Pro Val ----- Arg Ser Pro Lys Lys
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562 Lys Gly Ser Thr Thr Arg Val Ala Ser Thr Ala Asn Ala Glu Thr Glu Ala Thr Ser Ala 581
1894 -----CAGACCAATCTCATAACAGCAAGAGCTACATTCACCTGGA--- 1935
582 Phe Glu Thr Glu Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Val Tyr 601
1936 -----ATACAGAGTCAAAAGACTGAGTCTTASGCTATTTTAAAGAAAGSTCAI 1989
582 Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Ser Glu His Pro Glu 621
1989 -----ATGAGATGTTTCAAAAGAG 2046
582 Leu Glu His Ile Ile Thr Thr Leu Phe Glu His Thr Leu Glu Asn Glu Tyr Glu Leu Met 641
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2227 ACACAGGATATACAGAGCTCTCTGCTGAAAAGTATCCACAGAGTTGCGCATATAAT 2286
691 ----- 691
2287 AAAAATATAAATGATGACTTTTCAATGATAGATTGTGCTTAGAGATGCTACAAAANCA 2346
692 -----Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn 703
2347 GCTGATCTTTTCAGTGAAGAAATCAAAAGAAAGAAAGTATATATAAATTTTAA 2406
704 Ser Val Phe Met Glu Arg Leu Lys Thr Asn Ile Leu Glu Tyr Ala Ser Thr Arg----- 721
2407 ACAATAATAGTAGCAAGATCAAGTCACTGACGAAATACGACCTGCGGCAACAGAG 2456
722 -----Pro Thr Leu Ser Pro Ile Phe Pro His Ile Pro Arg Ser Pro Tyr Lys 737
2457 CATATGATGATGATGCTGACACTCTCTCTTCCACATATTAACCAACAG----- 2517
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2518 -----CAAGATCAAGAGAGAGATTTGGTAGAGAGAGCTGAAATTAAT 2562
757 Ser Pro Tyr Lys Ile Ser Glu Gly Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg 776
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777 Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Ile Lys Ile Asn Glu 796
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797 Met Val Lys Asn Ser Asp-----Arg Val Leu Lys Arg Ser Ala Glu Cys 811
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812 Ser Asn Pro Pro Lys 816
2719 GAAAGCCCGCCAAA 2733
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Search completed: January 19, 2003, 05:21:14
Job time : 148.718 secs

REF ID: A66531

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TEACHER: HAKA TERISTIS

1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26

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Journal of Management Education

1. Introduction

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Fig. 16. 1) 10; 2) 12; 3) 14; 4) 16; 5) 18; 6) 20; 7) 22; 8) 24; 9) 26; 10) 28; 11) 30; 12) 32; 13) 34; 14) 36; 15) 38; 16) 40; 17) 42; 18) 44; 19) 46; 20) 48; 21) 50; 22) 52; 23) 54; 24) 56; 25) 58; 26) 60; 27) 62; 28) 64; 29) 66; 30) 68; 31) 70; 32) 72; 33) 74; 34) 76; 35) 78; 36) 80; 37) 82; 38) 84; 39) 86; 40) 88; 41) 90; 42) 92; 43) 94; 44) 96; 45) 98; 46) 100.

MS 020470.01 (1869)

1. *Chlorophyll a* (Chl *a*)

1 Metabolically

[illegible]

14	67	CATAAAGTTCCTTAACCTAATAAGGAAAATGCATACCAGCATGCCCAAGATTGATAATGGTTATGT	126
QY	149	SerArgLeuLeuIysValTyrAspValLeuPheAlaLeuPheSerLysLeuGluArqThr	168
DG	127	TCAAAGTGTGTGAAGAATATCATCTATTGTTTGACTTTTAAAGAAATTTGAAAAAGACA	186
QY	169	CysGlnLeuLeuIleTyrLeuThrGlnProSerSorMet-----	181
DG	187	TGTGAATTTATATATTGACACACAGCCAGCAGCTGTGATATGATGTAATGAAATATAATTTCGA	246
QY	181	-----	181
DG	247	TGGCGTTAAAGCTTCTTCGGATCACATTTTTATTACCTAAAGCGGAAGCTATTACAAATC	306
QY	181	-----	181
DG	407	GAAAGATGATCTGTGTAATTTTCATTTTCAGTTAAATGCTATGTGCTCTGACTATTTTATTATA	366
QY	182	-----	182
DG	467	CTCTGACTGCAATGCTGTGCTCAAGAACCATATAAAGCAGCTGTTATACCAATTAALGGT	426
QY	190	SerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGlu	209
DG	427	TCACCTGACACACCCAGCGAGGTCAGAACACAGGAGCTGCACGCATACCAAAACAACATAGAA	486
QY	210	AccArgPheArgIleIleLeuValValCysTyrAspLysGlnCysAspIleAspGluVal	229
DG	487	AATGATACAAAGAAATTAITCAAGTTCTTGTAAACAAATGAATGATGATGAGTAGAGSTGT	546
QY	230	LysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuCylLeuValThrSer	249
DG	547	AAAAATGTTAATTCAAAAATTTTAACCTTTTAIGMAATCTCTTGCACTTGTAACATCT	606
QY	250	AcetylProProCysValGlnAsnLeuSerLysArgTyrGlnGlnIleTyrLeuLysAsn	269
DG	607	AATGGACTTCCACAGGTGTGAAAATCTCTCAACGCATACGACAGAAATTAATCTTAAAAAT	666
QY	270	LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIle	289
DG	667	AAAGATCTATATGCACAAATATTATTTTGGATATCATATAAAATTTTAAATGATATA	726
QY	290	AspSerPheGlnThrGlnArgThrProArgLysSerAsnLeuAspGlnGluValAsnVal	309
DG	727	GAAATGTTTGAACAACAAGASAAATACACAAAAGAAATAACTGTAISGAAGAGTGAATGTA	786
QY	310	IleProPheIsthThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIle	329
DG	787	ATTCTCTACACATCCACATAGGAGCTGTTAAGAACATATCCAACAAATTAATCATGATT	846
QY	330	LeuAsnSerAlaSerAspGlnProSerGlnAsnLeuIleSerTyrPheAsnAsnCysThr	349
DG	847	TTAAATTCACAAAGTAATCAATTTTAAAGAAATCGATTTCATTTTAAATTAATTCACAA	906
QY	350	ValAsnProLysGlnSerIleLeuLysArgValLysAspIleCglyTyrIlePheLysGlu	369
DG	907	GTGAATCCAAAGAAAGATATAATTAATAATATGAAGATATAATATATATATATATATAT	966
QY	370	LysPheAlaLysAlaValGlyGlnCysValGlnIleLysSerGlnArgTyrLysLeu	389
DG	967	AAATTTGCTAAACCTGTGGACACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1026
QY	390	GluValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGlnGluGluArqLeu	409
DG	1027	GGAGCTGATTTTATTATGAGTAAATGAAATGATGTTAAATCAGAGAGAGAACCATTA	1086
QY	410	SerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAla	429
DG	1087	TGCATTCAAAATTTTASCAAACTCTGATGCAACATTTTTCATATGCTCTTATTGGCG	1146
QY	430	CysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer	449
DG	1147	TGCGTCTTCAGGTGTGAATGCCACATATACGACAACTACATCTCGAAGATTTGATCT	1206

Oy	450	GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaIleAspPhe	489
Db	1207	GRAACAAITGTCTTCCCATGGATTTGAATGTCATAATTAAAAGCGTTTGATTTT	1266
Oy	470	TyrLysValIleGluSerPheIleLysAlaCylGlyAsnMetCysThrArgGlnMetIleLys	489
Db	1267	TATAAAGTCATCAAGAATTTTAACAAGCCAGAAGGCCTACTTGCACAGAGAAATGAAAA	1326
Oy	490	IleLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTyrLeuSerAspSerPro	509
Db	1327	CATTACAAATGATGCACATCGAAATGACGAATGCCATGCCATGGCTCTCACATTCACCT	1386
Oy	510	LeuPheAspGluIleLysGlnSerLysAspAlaGluGlyProThrAspHisLeuGluSer	529
Db	1387	TTATTTCATCTTATTAAATTAAGSANTGSAAGSAGCAATGATGACGCTTGAAATCT	1446
Oy	530	AlaCysProGluAsnLeuProGluGlnAsnAsnHisThrAlaAlaaspMetTyrLeuSer	549
Db	1447	CGTTGTCCTTAATCTCTCTCTCCAGATAATACACATCGACAGTAGAGATGATCTCTCT	1506
Oy	550	ProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla	569
Db	1507	CGTGAAGATCTTAAGSAAAAAGAGTCTCAATTAAGSGTGTAATATCTATCTGAAAATGCA	1566
Oy	570	GluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSer	589
Db	1567	GAGACATCAATCTAGATTTCTTACAGATTAAGATTAAGAGGATATGAAATATATATCTCTCT	1626
Oy	590	IlePheTyrLysValTyrArgLeuAlaTyrLeuAlaTyrLeuAspSerThrLeuCysSchuArg	609
Db	1627	CTGTCTTATAAAAGCATGATCGCTTAGCTCATCTCCGGCTAAATACACTTGTGCAAGCG	1686
Oy	610	LeuLeuSerGluHisProGluLeuGluHisIleIleTyrThrLeuPheGluHisThrLeu	629
Db	1687	CTCTGTCTGAGCCCCAGAAITAGAACATATCATCTGGACCCTTTTCCACGACACCCCTG	1746
Oy	630	GlnAsnGlnTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMet	649
Db	1747	CAGAAATGATTAATCAAT	1806
Oy	650	TyrCylTrpCysLysValLysAsnIleAspLeuLysPheLysIleIleValIleAlaTyr	669
Db	1807	TATGATATATCAATCAAGCAATATAGACTTAAATTCAAAATCAATGTAAACATCAAC	1866
Oy	670	LysAspLeuProHisAlaValGlnGlnThrPheLysArgValLeuIleLysGluGluAla	689
Db	1867	AAGGATCTTCTCATCTCTTCCAGAGATATCAAAAGCGTTTGCATCAAGSAGACAGAG	1926
Oy	690	TyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysIleAsnIle	709
Db	1927	TATGATCAT	1986
Oy	710	IleGlnTyrAlaSerThrAlaPheProThrLeuSerPheIleProHisIleThrArgSer	729
Db	1987	TGTAGATATCTCTCAAG	2046
Oy	730	ProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPro	749
Db	2047	CGTTACAAAGTTCCTAGTTCAGCTTACGATTCCTGCGAGGAGACATCATATATTCACCC	2106
Oy	750	LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg	769
Db	2107	CTAAGSAGATATATATAAATTTTAAAGATATATATATATATATATATATATATATAT	2166
Oy	770	SerArgIleLeuValSerIleGlyGlnSerPheGlyThrSerGlyLysPheGlyLysIle	789
Db	2167	TCAAGAAATCTTACATCAATCTGTAATCTGAGGAGCTTCTGACAGCTTCTCAAAAAIA	2226
Oy	790	AsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluCylSerAspPro	809
Db	2227	AATCACATGCTATCTAACAATCAAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2286


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450 GlyThrAspLeuSerPheProIleLeuAsnValIleuAsnLeuIysAlaPheAspPhe 469
1000 GSAACAGATTTGCTTTCCCATGATCTCAATGCTTAATTTAAAGACCTTGATTT 1971
470 TyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLys 489
1000 IACAAAGTGAATCAAACTTTTATCAAGCAACAAGGCAACTTTCACAAGAGAAATGATAAAA 1911
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1000 CATTTAGAACATATGTAATATGAAATCTTCTATGCTTCTTCAATGCTTCAATGCTT 1851
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1000 GCTGTAAGATCTCTAAAGCAAAAGATTTAAATACAGAGTAAATCTCTCTCTCTCTCTCT 1671
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950 CCTAAACCACTGAAAGAACTACCTTTTGAATATGAGAGATCACATGCAACACATGCAAG 891
960 LysHisLeuProLysLysSerLysPheGlnIleLysLeuAlaGluMetThrSerThrArg 849
970 AAACATCTCCAGAGAGAGTCCAAATTTTCAGCAGCAAACTGCCAGAAATGACATCTCTACT 831
980 ThrArgMetGlnLysGlyLysMetAspSerMetAspThrSerAsnLysGluGluLys 869
990 AATGGAATGTAAGAAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771

RESULT 10
US-08-470-091-1
: Sequence 1, Application US/08470091
: Patent No. 5912236
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: APPLICANT: Hu, Shi-Xue
: APPLICANT: Benedict, William F.
: TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
: TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/470,091
: FILING DATE: JUN-16-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: FILING DATE: US/08/038,760
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,452
: REFERENCE/DOCKET NUMBER: 7409 025-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PUNNIF
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3232 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 19..2469
: US-08-470-091-1

Alignment Scores:
Pred. No.: 0 Length: 3232
Score: 3870.50 Matches: 759
Percent Similarity: 92.58% Occurrence: 1
Best Local Similarity: 92.56% Mismatches: 1
Query Match: 85.97% Indels: 59
DB: 2 Gaps: 1

US-09-026-459a-47 (1 869) x 23 08 470 025-1 (1-2232)
OY 109 AspLeuAspGluMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerVal 128
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1d	7	GACATACAAGCAGACGACGGCTTTCATTCTACGACTACACAAAAACAACAAAACACGTGC	66
QY	129	HISLysPhePheAsnLeuLeuLysGLuILEAspThrSerThrLysValAspAsnAlaMet	148
1d	67	CATAAAATTTTAATTAATAAAGCAATTCATACAGTACAAAGGAGAAAGCGATG	126
QY	149	SerArgLeuLeuLysLysValLeuPheAlaLeuPheSerLysLeuGluArgThr	168
1d	127	TCAAGAATGCTGAAGAAATGATGATGTTTGTCATCTCTCACGAATTTGAAAGGAC	186
QY	169	CysGlnLeuILETyLeuThrGLuProSerSerSerMet	181
1d	187	TCGCAAACTAATAATTCACAAACAACCCACACAGCTCGAATACAGAACAAATCTGCCA	246
QY	181	-----	181
1d	247	TTCTGTCAAAAGTTCTTGTAATACATTTTTATATAGCTAAGGCGAAGATTACAAATG	306
QY	181	-----	181
1d	307	GAAGATGCTGGTCATTTTAATTCAGTAAATGATGCTGCTGTGACTATTTATTATAA	366
QY	182	----- ValAlaValILLEProIleAsnGly	189
1d	367	CTCTCACTCCCATGCTCTCAACCAACATAAAAAACGCTGTATACCCATTAAGTGT	426
QY	190	SerProArgThrProArgArgLysAsnArgSerAlaArgILeAlaLysGlnLeuGlu	209
1d	427	TCACTCGAACACGACAGCGAGGTCAGAACAGGAGTCGACGATAGCAAAACACATGAA	486
QY	210	AsnAspThrArgILELeuValLeuLysLysGluHisGluCysAsnILLEAspGluVal	229
1d	487	AATATATCAAGAAATATTCGAATCTCTGTAAANANCATGAATGTAAATAGATGAGTG	546
QY	240	LysAsnValTYrPheLysAsnPheILEProPheMetAsnSerLeuGlyLeuValThrSer	249
1d	547	AAAAATGCTTATTCAAAAATTTTAACTTTTATGAATCTCTTGGACTGTGAACACT	606
QY	250	AsnILEProGluValGluAsnLysSerLysArgTYrGluHisILEtyrLeuLysAsn	269
1d	607	AATCGACTTCACAAAGCTTCTCAANAATAGAAAGAAATTAATCTTAAAAAT	666
QY	270	LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGluThrAspSerILE	289
1d	667	AAATCTCTGATGCAAGATTATTTTGGATCATGATATAAAATCTCTCAATGATCTATA	726
QY	290	AspSerPheGluThreILuArgThrProArgLysSerAsnLeuAspGluGluValAsnVal	309
1d	727	CACAGTTTTCAAAACAACAGAAACCACGAAAAAGTAACCTTAGAAGACGGTCAAIGTA	786
QY	310	IleProProHisThrProValArgThrValMETAsnThrIleGlnGluLeuMetILE	329
1d	787	ATTCTCTCAACAATCTCAATTAAGACTGTTATGAACAATATCTCAACAATTAATGATGAT	846
QY	330	PheAsnSerAlaSerAspLEuProSerGluAsnLeuILLESerTYrPheAsnAsnCysThr	349
1d	847	TTAAATTAAGCAAGTGATTAACCTTCAAAAAATCGATTGCTATTTTAAACATGACACA	906
QY	350	ValAsnProLysLysSerILELeuLysArgValLysAspILEGlyTYrILEPheLysGlu	369
1d	907	GTCAATCTCAAACTAAAGTAATACAAAAACATGAAAGCATATACATATATCTTAAACAG	966
QY	370	LysPheValLysAlaValILEGluGlyCysValILEuILEglySerGluArgTYrLysLeu	389
1d	967	AAATTTCTTAAACATGTGGACAAAGTTGTCTGTGTGAAATTTGATGACACACATATAA	1026
QY	390	GlyValArgLeuArgTYrArgValMETGluSerMetLeuLysSerGluGluGluArgLeu	409
1d	1027	GGATTTCTGTGATTAATACGAATATGNAATATGCTTAATATAGAAAGAAAGACGATTA	1086
QY	410	SerILEAsnAspPheSerLysLeuLeuAsnAspAsnILEPheHisMetSerLeuLeuAla	429
1d	1087	TCATATCAAAATTTTAACTAAATTCGAAACGAAACATTTTCAATATCTATATGCCC	1146

QY	430	CysAlaLeuGluAlaValMetAlaThrTyrSerArgSerThrSerGluAsnLeuAspSer	449
DB	1147	TGGCTCTTGAGCTGTGAATGGCAATATAAGACAAATATATCAAAATTTTATCTT	1206
QY	450	GlyThrAspLeuSerPheThrTrpLeuAspValLeuAsnLeuLysAlaPheAspPhe	469
DB	1148	TT	1207
DB	1207	GGAAACAGATTTGGCTTTCCCAACGATTTGCAATGGCTTAATTTAAATCAAAAGCTTTCATTTT	1266
QY	470	TyrLysValIleGluSerPheIleLeuAlaLeuGluGlyAsnLeuThrArgLysMetTrpLys	489
DB	1267	TACAAATGCAACCAAGCTTTTCACAAGACACAAAGGCAATTTGACAAACAGAAATCAAAAA	1326
QY	490	HisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerPro	509
DB	1427	CATTAGAAAGATGTGAATATGGAATCATGAAATCTTTGATGCTTTGATATTATTCAT	1486
QY	510	LeuPheAspLeuIleGlyGlnSerLysAspArgLeuGlyProIleAspHisLeuMetSer	529
DB	1487	TTATTTCATCTTATTAACCAATCAAGGACACAGAAACAAATGATCAATTTTCAATCT	1546
QY	530	AlaCysProLeuAsnLeuProLeuGluAsnAspHisThrAlaIleAspMetTyrLeuSer	549
DB	1447	GCTTGTGCTCTTAAATCTCTCTCTGAGAAATAACATCATGCAATATGCAATATTTCT	1506
QY	550	ProValArgSerProLysLysCysLysSerThrThrArgValAsnSerThrAlaAspAla	569
DB	1507	CTGTATAGATCTCCCAAGAAAGAAAGAGTTCATCTAGCTGGTAAATTTTATCTGAAATGCA	1566
QY	570	GluThrGlnAlaThrSerAlaPheGlnThrGluLysProLeuLysSerThrSerLeuSer	589
DB	1567	GAGACACAAACCAACCTCAGGCTTCCAGATCCAGACAGCAAGCCATCAAAATACATCTTCTCA	1626
QY	590	LeuPheTyrIleLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuLysGluArg	609
DB	1627	CTGTCTTATAAAAAGATGATCGGTAGCGTATCTCCGCGCTAAATATACCTTTCGCAACGC	1686
QY	610	LeuLeuSerGluHisProGluLeuGluHisIleIleThrThrLeuPheGlnHisThrLeu	629
DB	1687	CTTCTGTCTGACACACACAGAAATAGAAATATATCATCTGTGAACTTTTCTCCAGCAATCTG	1746
QY	630	GluAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetLysSerMet	649
DB	1747	CAGAAATGAGTATCAACTTCATGACACACAGCAATTTGCAATAAATATGATGCTGTTCATG	1806
QY	650	TyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyr	669
DB	1807	TATGGCAATGCCAAGTGAAGAAATATAGACTTTAAATTTAAAAATATTTCAACCAATATCT	1866
QY	670	LysAspLeuProHisAlaValGluGlnIleThrPheLysArgValLeuIleLysGluGluGlu	689
DB	1867	AAGCATCTTCTCATGCTGCTTCACAGAGAAATTCACAAACGGTTTTCATCAAAATACAGAG	1926
QY	690	TyrAspSerIleIleValPheTyrAsnSerValPheMetGlnAlaGluCysThrAsnIle	709
DB	1927	TATGATTTCTATATATAGATTTCTATAACATGGCTCTTCATGACACATCAAAATAAT	1986
QY	710	LeuGluTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArgSer	729
DB	1987	TTCCAGATATCTTCCACCGCGGCGCTATCTTCTCATCAATATCTCAATATCTCTCAAGC	2046
QY	730	ProTyrLysPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSerPro	749
DB	2047	CCATTCAAGTTTCTAGTTCAGCTTATGAGATCTCTGAGAGCAATATCTATATTATTCAT	2106
QY	750	LeuLysSerProTyrLysIleSerGluLysLeuProThrProIleLysMetThrProArg	769
DB	2107	CTCAAGACATCAATAAAATTTCACAAGAGATCTGCCCAATCAATCAATATCTCTCAAGC	2166
QY	770	SerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheIleLysIle	789
DB	2167	TCAAGAAATCTATATCAATTTGCTCAATATCTCGAGATCTCTGCAACATTCATCAAAATAT	2226

[illegible]

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100 2150 TCAATGAAAAATTTTAAAGTATGAAATGACAAATTTTCAATGATGTTATGGCG 2051
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102 400 CysAlaLeuGluValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 449
103
104 2090 TGGTCTTGAGATGATGAAATGATATAGTAAATAGCAAGCACTACATCTAGAAATCTTGATTC 2031
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106 450 GlyThrAspGluSerPheProTrpTyrLeuAsnValLeuAsnLeuCysAlaPheAspPhe 469
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108 2040 GAAAGATATGCTTTTCTGATGATTCGAAATGATGATTTAAATTTAAAGATCTTGATTTT 1971
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110 470 TyrLysValTyrLeuSerPheTyrLeuGluGluGluGluGluGluGluGluGluGlu 489
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112 1970 TACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
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114 490 HisLeuGluAlaCysGluHisAlaTyrMetGluSerLeuAlaTrpLeuSerAspSerPro 509
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116 1910 CATTATCAACCAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1851
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118 510 LeuPheAspLeuTyrLysGluSerLysAspArgGluGluGluGluGluGluGluGluGlu 529
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120 1850 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1791
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122 540 AlaTyrProLeuAsnLeuProLeuGlnAsnAspHisThrAlaAlaAspMetTyrLeuSer 549
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124 1790 GTTGTGCTGCTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1731
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126 550 ProValAlaSerProLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 569
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128 1730 CTCTGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1671
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130 570 GluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuGluGluGluGluGluGlu 589
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132 1670 GAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1611
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134 590 LeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArg 609
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136 1610 CTGTTTATAAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1551
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138 610 LeuLeuSerGluHisProGluLeuGluHisLeuTrpThrLeuPheGluHisThrLeu 629
139
140 1550 CTCTGCTGAGACACACAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1491
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142 640 GlnAsnGlnTyrGluGluMetArgAspArgHisLeuAspGlnIleMetMetCysSerMet 649
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144 1490 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1431
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146 650 TyrGlyThrCysLysValTyrAsnTyrAspTyrLysPheTyrLeuValThrAlaTyr 669
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148 1430 TATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1371
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150 670 LysAspLeuProHisAlaValGluGluThrPheLysArgValLeuLeuLysGluGluGlu 689
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152 1370 AAGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCA 1311
153
154 690 TyrAspSerThrLeuValPheTyrAspSerValPheMetGlnArgLeuLysThrAsnIle 709
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156 1310 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1251
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158 710 LeuGlnTyrAlaSerThrArgProProThrLeuSerProThrLeuHisIleProArgSer 729
159
160 1250 TGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1191
161
162 740 ProTyrLysPheProSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPro 749
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164 1190 CATTATCAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1131
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166 750 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 769
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168 1130 CTGAAATGCTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1071
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171

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100 1070 TCAAGAACTTAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1011
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102 750 AsnGlnMetValCysAsnSerAspArgValIleLeuLysArgSerAlaLeuLysSerAspPro 809
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104 1010 AATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
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106 810 ProLysProLeuLysLysLysLeuArgPheAspIleGluLysSerAspIleAlaAspLysSer 829
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108 950 CTTAAACGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 891
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110 830 LysHisLeuProGlyGluSerLysPheGluGluLysLeuAlaGluMetThrSerThrArg 849
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112 890 AAAATCTCTCCAGAGAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 841
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114 850 ThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysLysLysLys 869
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116 840 ACAGCATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAA 771
117

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RESULT 12

US-08-842-883-1
Sequence 1, Application US/08842883
Patent No. 5807681

GENERAL INFORMATION:

APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
OF CANCER
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSER: SELDEL, GONDA, LAVORGNA & MINATO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/842-883

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4853 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 70..3489

US-08-842-883-1

Alignment Scores:

Prod. No.: 5,48e-65 Length: 4853
Score: 756.50 Matches: 274
Percent Similarity: 46.98% Conserved: 172
Best Local Similarity: 22.72% Mismatches: 441
Query Match: 16.80% Indels: 419
DB: 1 Gaps: 49

US-09-026-459A-47 (1-869) x US-08-842-883-1 (1-4853)


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QY 598 -----GlySerThrThrArgValAsnSer----- 565
Db 2179 GTCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2238
QY 596 -----ThrAlaAsn----- 568
Db 2239 GACACAGATTTTGGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2298
QY 598 ----- 568
Db 2299 ACCATTCTGTCGAAGATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 2358
QY 599 -----AlaGluThrGlnAla-----ThrSerAlaGluGln----- 578
Db 2359 GTCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2418
QY 578 ----- 578
Db 2419 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2478
QY 578 ----- 578
Db 2479 GAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2538
QY 579 -----ThrGlnIleProLeuIleSerThrSerLeuSerLeuGluIleVal 595
Db 2539 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2598
QY 596 TyrArgLeuAlaTyrLeuAlaLeuAsnThrLeuGlnIleSerThrSerLeuGlnIleVal 614
Db 2599 TACATTTTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2655
QY 615 ProIleLeuGlnIleSerThrLeuGlnIleSerThrLeuGlnIleSerThrLeuGlnIleVal 634
Db 2656 GAAATGAGAAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2712
QY 635 LeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLeu 654
Db 2712 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2772
QY 655 ValIleAsnIleAspLeuIleValIleValThrAlaTyrLeuGlnIleSerThrLeuGlnIleVal 674
Db 2772 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2832
QY 675 AlaValGlnIleThrPheTyrArgValIleLeuIleVal 686
Db 2832 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2892
QY 686 ----- 686
Db 2892 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2952
QY 686 ----- 686
Db 2952 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3012
QY 687 -----GluGluGlu 689
Db 3012 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3072
QY 690 TyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgIleCysThrAsnIle 709
Db 3072 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3132
QY 710 LeuGlnTyr-----AlaSerThrArgProProThrLeuSerProIleProHisIlePro 727
Db 3132 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3192
QY 728 ArgSerProTyrIlePheProSerSerProLeuArgIle-----ProGlyGlyAsn 744
Db 3192 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3252
QY 744 ----- 744

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QY 745 IleTyrIleSerProLeuLysSerProTyrLeuLysIleSerGluIleLeuProThrProThr 764
Db 3235 GTCACATTTCCCAACAAAAA-----GAAACA 3264
QY 765 LysMetThrProArgSerArgIleLeuValSerIleGlyIleSerThrSerGlu 784
Db 3265 ATGCTTCTCTCGAGAAAGATTTTCTATTACTTTAAACACT-----CTTCAAG 3318
QY 785 LysPheGlnLysIleAsnGlnMetValIrySAsnSerAspArgValLeuLysArgSerAla 804
Db 3319 AGATGAGAGAAATTAATGATGATA-----GAGACAGA 3354
QY 805 GluIleSerAsnProProLysProLeuLysLeuArgPheAspIleLeuLysSerAsp 824
Db 3355 GAA-----ACTCTTACTAAACAGAGAGAAATTTCTTTGGAAATGGAAT 3399
QY 825 GluAlaAspGlySerLysHisLeuPro-----GlySerLeuLysPheGlnIleLysLeuAla 844
Db 3400 GAATCAGCTGCAAAAGAAATTTGGCCAGAAAAATCATTTGCTTATTATAGGCTCTGAA 4459
QY 844 GluMetThrSerThrArg 849
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RESULT 13

US-08 842-877-1

Sequence 1, Application US/08832877

Patent No. 5840506

GENERAL INFORMATION:

APPLICANT: Giordano, Antonio

TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF

TITLE OF INVENTION: CANCER

NUMBER OF SEQUENCES: 116

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.

STREET: Suite 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER RELEASABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/832,877

FILING DATE:

CLASSIFICATION: 4.6

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 8421 14 US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8483

TELEFAX: (215) 568-5549

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4853 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 70..3489

US-08-842-877-1

Alignment Scores:

Pred. No.: 5,480-65

Score: 756.50

Percent Similarity: 36.98%

Length:

Matches:

Conservative: 172

US-07-708 962 1

Alignment Scores:

Prod. No.: 3,450-62 Length: 2909
 Score: 724.50 Matches: 238
 Percent Similarity: 38.41% Conservative: 125
 Best local similarity: 25.19% Mismatches: 265
 Query Match: 16.09% Indels: 317
 Gaps: 27

US-09-026 459A 47 (1-869) x US-07-708-962-1 (1-2808)

QY 121 GlnLysAsnIleuLysSerValHisLysPheAsnLeuLysGluIleAspThr 140
 DB 121 GlnLysAsnIleuLysSerValHisLysPheAsnLeuLysGluIleAspThr 140
 DB 88 CAGAGGAGGATTTCCTGCGGATGCTTAAGGATCTGCTTAATTCCTGCTGACACATTTTCCT 147
 QY 141 SerThrLys -----ValAspAsnAlaMetSerArgLeu 151
 DB 141 SerThrLys -----ValAspAsnAlaMetSerArgLeu 151
 DB 148 TATA-TAAGGTAATTTTGGATGATGGGATGATTTAGTAAGCTCTTATCATTTACTT 207
 QY 152 LeuLysValLeuPheAlaLeuPheSerLysLeuCysArgThrCysGluLeu 171
 DB 152 LeuLysValLeuPheAlaLeuPheSerLysLeuCysArgThrCysGluLeu 171
 DB 208 CTATGCTGCTGCAATGATCTTTCGCAATGCGGATTTATGCGGCAAAATACAGAGACTTIG 267
 QY 172 IleTyrLeuThrGlnProSerSerSerMetValAlaValIleProIleAsnGlySerPro 191
 DB 172 IleTyrLeuThrGlnProSerSerSerMetValAlaValIleProIleAsnGlySerPro 191
 DB 268 CTA -----AATCCATCA-----TTTAAAGCTTTACCA 294
 QY 192 ArgIleProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAsp 211
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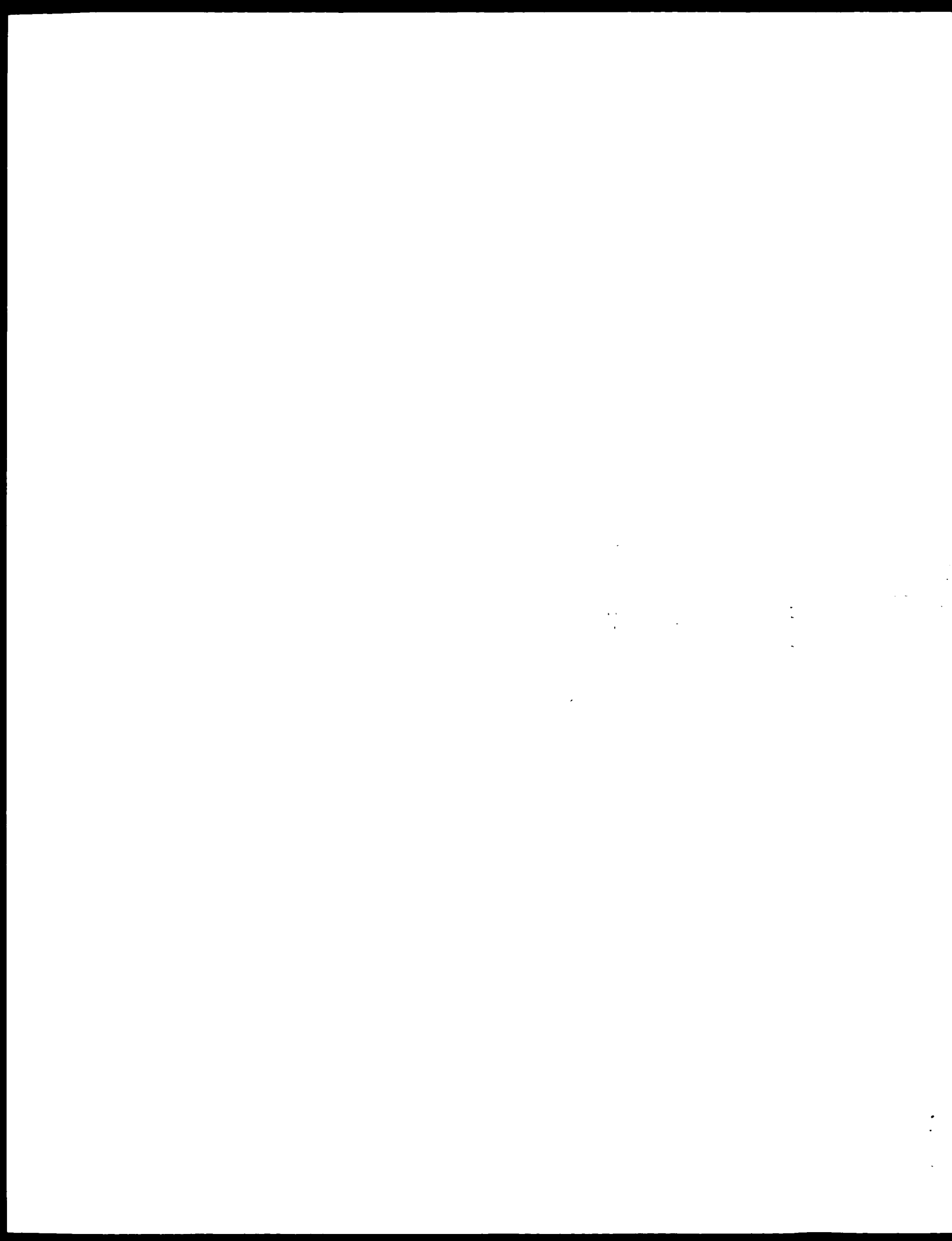
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Search completed: January 19, 2003, 05:45:40
 Elapsed time: 168.44 secs



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RESULT 4
US-09-315-113-3
Sequence 3, Application US/09315113
Patent No. 6,979,927
GENERAL INFORMATION:
APPLICANT: Antelman, Douglas
Gregory, Richard J.
Wills, Kenneth N.
TITLE OF INVENTION: Tissue Specific Expression of
Retinoblastoma Protein
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,113
FILING DATE: 19 May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,092
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FILLIS, Penelope A.
REGISTRATION NUMBER: 35,136

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: RESULT 6
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: Sequence 1, Application PC/PUS9410357
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: CLINICAL INFORMATION:
:
: REFERENCE: The Regents of the University of California
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: APL/PLANT: dsc Gadj, Inc.
:
: TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
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: TITLE OF INVENTION: Susceptibility Gene Prodigy+

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: FGT/US94/18357
FILING DATE: 13-SEP-1994

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110 RESULT 8
111 US-08-048-760-1
112 : Sequence 1, Application US/08048760
113 : Patent No. 5496731
114 : GENERAL INFORMATION:
115 : APPLICANT: Xu, Hong-Xi
116 : APPLICANT: Xu, Shi-Xue
117 : APPLICANT: Benedict, William F.
118 : TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
119 : TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy
120 : NUMBER OF SEQUENCES: 3
121 : CORRESPONDENCE ADDRESS:
122 : ADDRESSEE: Pennie & Edmonds
123 : STREET: 1155 Avenue of the Americas
124 : CITY: New York
125 : STATE: New York
126 : COUNTRY: U.S.A.
127 : ZIP: 10036-2711
128 : COMPUTER READABLE FORM:
129 : MEDIUM TYPE: Floppy disk
130 : COMPUTER: IBM PC compatible
131 : OPERATING SYSTEM: PC-DOS/MS-DOS
132 : SOFTWARE: PatentIn Release #1.0, Version #1.25
133 : CURRENT APPLICATION DATA:
134 : APPLICATION NUMBER: US/08/048,760
135 : FILING DATE: 1993/03/25
136 : CLASSIFICATION: 424
137 : ATTORNEY/AGENT INFORMATION:
138 : NAME: Polissant, Brian M
139 : REGISTRATION NUMBER: 28,462
140 : REFERENCE/DOCKET NUMBER: 7409-025-999
141 : TELECOMMUNICATION INFORMATION:
142 : TELEPHONE: (212) 790-9090
143 : TELEFAX: (212) 869-9741/8864
144 : TELEX: 66141 PENNIE
145 : INFORMATION FOR SEQ ID NO: 1:
146 : SEQUENCE CHARACTERISTICS:
147 : LENGTH: 4242 base pairs
148 : TYPE: NUCLEIC ACID
149 : STRANDEDNESS: double
150 : TOPOLOGY: not relevant
151 : MOLECULE TYPE: DNA
152 : FEATURE:
153 : NAME/KEY: CDS
154 : LOCATION: 19..2469
155 : US-08-048-760-1
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157 Alignment Scores:
158 Pred. No.: 0 Length: 4242
159 Score: 3863.50 Matches: 764
160 Percent Similarity: 93.05% Gaps: 0
161 Best Local Similarity: 93.05% Mismatches: 0
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RESULT 9

US 09 026 459a 2/2

Sequence 2, Application US/08048760

Patent No. 5496741

GENERAL INFORMATION:

APPLICANT: Xu, Hong Ji

APPLICANT: Xu, Shi Xue

TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and

METHODS FOR Tumor Suppressor Gene Therapy.

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edwards

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10046-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: pc/bs2/ms dos

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/048,760

FILING DATE: 19940425

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 7409-025-959

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 740 9090

TELEFAX: (212) 869 9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4242 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

Topology: not relevant

MOLECULE TYPE: DNA

US 09 026 459a 2

US 09 026 459a 2

US 09 026 459a 2

US 09 026 459a 2

US 09 026 459a 2

US 09 026 459a 2

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US 09 026 459a 2

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 DB 3050 TGTCAACTTATATATTTGACCAACGCGAGTGTGATATCTATGAAATATATTTGCA 2991
 QY 189 LeuValLeuLysValSerIleThrPheLeuLeuAlaLysGlyGluValLeuGluMet 208
 DB 2990 TTGGTGTGAAAAGTTCTTGGATACATTTTATTTATTTATTTATTTATTTATTTATTTATTT 2931
 QY 209 GluAspLeuValIleSerPhePheLeuMetLeuLysValLeuAspThrPheIleLys 228
 DB 2940 GACACATCATCTGGTGTGCTTCAAGAAATATATATATATATATATATATATATATATAT 2871
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 DB 2870 CTCCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2811
 QY 243 Ser 243
 DB 2810 TCACCTCGAATACCCACAGGAGGTGACAAAGAGAGTGTGAGAGTGTGAGAGTGTGAG 2751
 QY 243 243
 DB 2750 AATGATACAGAAATATATGAACTTCTGCTTAAATCAATATGAACTTCTGCTTAAATCA 2691
 QY 244 244
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Alignment Scores:
 Pred. No.: 0 Length: 4242
 Score: 484.50 Matches: 763
 Percent Similarity: 94.05% Conservat: 0
 Best Local Similarity: 94.05% Mismatches: 0
 Query Match: 85.94% Indels: 57
 Gaps: 2

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QY 472 TyrLysValIleLeuSerPheLysAlaGluGlyAsnLeuThrArgGluMetLys 491
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DB 753 GCTTAAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
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RESULT 10
US-08-470-091-1
: Sequence 1, Application US/08470091
: Patent No. 5912246
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: APPLICANT: Hu, Shi-Xue
: APPLICANT: Benedict, William F.
: TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
: METHODS FOR Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/470,091
: FILING DATE: JUN-16-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/038,760
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M
: REGISTRATION NUMBER: 28,462
: REFERENCE/KEY NUMBER: 7439-925-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3242 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..2459
US-08-470-091-1
Alignment Scores:
Pred. No.: 0 Length: 3222
Score: 3863.50 Matches: 763
Percent Similarity: 93.0% Conservative: 0
Best Local Similarity: 93.0% Mismatches: 0
Query Match: 85.93% Indels: 57
DB: 2 Gaps: 2
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DB 110 TATGATGCTTATTAAG 128

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 167 HisLeuSerPheAsnLeuLeuLysGluLeuAspThrSerThrLysValAspAsnAlaMet 148
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 169 CATAAATCTTAACTTACAAAAGAAATGATACAGTACAAATGATATATGCTATG 126
 170 SerArgGluLeuLeuLysGluLeuAspValLeuPheAlaLeuPheSerLysLeuGluArgThr 168
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 176 GluAspAspLeuValLeuSerPheGlnLeuMetLeuGlyValLeuAspThrPheLeuLys 228
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 180 SerProMetLeuLeuLeuLysGluLeuLysGluLeuLysGluLeuLysGluLeuLysGlu 243
 181 TCACTCTGAAACGACAGAGGTCAGAAACAGAGGTCAGAGGTCAGAGGTCAGAGGTCAGAG 486
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 183 AsnSerLeuGlyLeuValThrSer 251
 184 AAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
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 187 LysAspLeuAspAlaArgGluPheLeuAspHisAspLysThrLeuGlnThrAspSerTrp 291
 188 AAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
 189 AspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluLeuValAsnVal 311
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 191 HisProGlnThrProValArgThrValMetAsnThrLeuGlnLeuLeuLeuLeuLeuLeuLeu 331
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 197 LysPheAlaLysAlaValGluGluLysValGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 491
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 1867 AAGATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1926
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 1927 TATGATCTATATAGATCTATATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1986
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 732 ProLysPheProSerProLeuArgAlaLeuArgLysGlyAsnLeuLeuLysThrSerPro 751
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392 AsnGlnMetValGlyAsnSerArgValLeuLysArgSerAlaGlnIleLysSerAsnPro 811
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Sequence 1

US-09-026-459a-49

Sequence 2: Applicant: US-09-026-459a-49

Patent No. 5912236

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

APPLICANT: Xu, Shi-Xue

APPLICANT: Beaudet, William E.

TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and

TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennic & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPILED READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: pc-pro/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-026-459a-49

FILING DATE: JUN-16-1995

CLASSIFICATION: G16

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US-09-026-459a-49

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Polissant, Brian M.

REGISTRATION NUMBER: 38,462

REFERENCE/AGENT NUMBER: 7400-026-000

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 3232 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: not relevant

MOLECULE TYPE: DNA

US-09-026-459a-49

Alignment Scores:

Seq. No. 1 0 Length: 3232

Score: 3863.50 Matches: 763

Percent Similarity: 94.0% Mismatches: 0

Best Local Similarity: 94.0% Indels: 57

Query Match: 85.93% Gaps: 2

US-09-026-459a-49 (1-87) x US-09-026-459a-49 (1-3232)

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 272 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2571
 272 LysAspLeuAspGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 291
 2570 AATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2511
 292 AspSerPheThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 311
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 391 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
 392 GlnValArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 411
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 412 SerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAla 411


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1070 TCAAGAACTTCTAGTACAACTTGGTCAATCAATTCAGACATTCAGAAAGTCCAGAAAAA 1011
792 AsaGluMetValCysAspSerAspArgValIleuLysSerAspArgValIleuLysSerAspPro 811
1010 AATCAGATGGTATGTAAACAGGAGCGGTGGTCTAAAAGGAAGTGGTAAAGGAAATCAACCT 951
812 ProLysProLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 831
950 CCTAAACCACTGAAAAAAGTAACTGCTTTGATATTCAAGGAACTGAAAGAAAGAAAT 891
832 LysHisLeuProGlyGluSerLysPheGluHisLysLeuAlaGluMetThrSerThrArg 851
890 AAACATCTCCACAGACAGACAGCAATTTCCAGCAGAAATTCAGCAGAAATGAACTTTTAACTCA 841
852 ThrArgMetGluLysGluLysMetAspAspSerMetAspThrSerAsnLysLysLysLys 871
840 ACAAGATGCAAAAGCAAAATGAAATGATAGATGATATATCTTAAATGAAAGAAAGAAAA 771

RESULT 12
US-08-832-883-1
: Sequence 1, Application US/08842884
: Patent No. 5807681
: GENERAL INFORMATION:
: APPLICANT: Giordano, Antonio
: APPLICANT: Haidi, Alphonso
: TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
: OF CANCER
: NUMBER OF SEQUENCES: 115
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SHORL, GONIA, LAVAKONA & MUNACO, P.C.
: STREET: Suite 1800 Two Penn Center Plaza
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/832,884
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Monaco, Daniel A
: REGISTRATION NUMBER: 30,480
: REFERENCE/BOOKET NUMBER: 8321-14 US1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-8384
: TELEFAX: (215) 568-5549
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4853 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 70..4489
: US-08-832-883-1

Alignment Scores:
Pred. No.: 4,320-70 Length: 4853
Score: 801.50 Matches: 289
Percent Similarity: 37.06% Conservative: 159
Best Local Similarity: 23.90% Mismatches: 348
Query Match: 17.83% Indels: 423
Gaps: 1
US-09-026-459A-49 (1-871) x US-08-832-883-1 (1-4853)

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2150 TCAATCAAAAATTTTAAAGAAATTTTCAAAATCAATTTTCAATTTTATTTGGCG 2091
442 CysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGluAsnLeuAspSer 451
2090 TGGCTTTTGGAGTTGTAATGAGGCAATATAGCAGAAGTACATCTCAGAACTTCATTTCT 2031
442 GlyThrAspLeuSerPheProThrIleLeuAsnValIleuAsnLeuLysAlaIleuAspPhe 471
2040 GAAATGATTTGCTTTTCATGATTTGATGCTGTTAAATTTAAAAAGCTTTGATTTT 1971
442 TyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLys 491
1970 TATAAATTCATCAAAAGTTTATCAAAAGCAAGAGCAAGCTTCACACAGCAAAATGATAAAA 1911
442 HisLeuGluAlaArgLysIleHisArgIleMetGluSerLeuValArgLeuSerAspSerPro 511
1910 CATTTACAAACAGAGCAAAATCAAAATCAAGAACTCTGCAAGCTTCATTCACCT 1851
512 LeuPheAspLeuIleLysGluSerLysAspArgGluGlyProThrAspHisLeuGluSer 531
1850 TTAATTCATCTTATTAATCAATCAAGAGCAAGAGCAAGCTGATCAGCTTCAATCT 1791
532 AlaCysProLeuAsnLeuProGluGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSer 551
1790 GCTTCTCTCTTAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1731
552 ProValArgSerProLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 571
1740 CTCTTAAATCACTCCAAAGCAAAAGAGCTTCAACTACCGCTGTAATTTCTAACTTCAAAATCA 1671
572 GluThrGluAlaThrSerAlaPheGluThrGluLysProLeuLysSerThrSerLeuSer 591
1670 GAAAGCAAGCAAGCAAGCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1611
592 LeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArg 611
1610 CTCTTTTATAAAAAGCTTAACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 1551
612 LeuLeuSerGluHisProGluGluGluHisIleIleThrThrLeuPheGluHisThrLeu 631
1550 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1491
632 GluAsnLeuTyrGluLeuMetArgAspArgHisLeuAspGluIleuMetMetCysSerMet 651
1490 CAAGATGATGAGAAATCATGAGAGAGAGAGATTTGGATTTGGATTTGGATTTGGATTTG 1431
652 TyrGlyTyrCysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyr 671
1430 TATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1371
672 LysAspLeuProHisAlaValGluGluThrPheLysArgValLeuIleLysLysGluGlu 691
1370 AAGATGCTCTCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1311
692 TyrAspSerIleIleValPheTyrAsnSerValPheMetGluArgLeuLysThrAsnIle 711
1310 TATATTTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1251
712 LeuGluTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArgSer 731
1250 TCTAGTATGCTTCCAGTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1191
732 ProTyrArgPheProSerSerProLeuArgIleProGlyLysAsnIleTyrIleSerPro 751
1190 CTTTAAAGTTTCTAGTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1131
752 LeuLysSerProTyrLysLysSerGluGluProIleProIleLysMetThrProArg 771
1130 CTGAAGATGCTATATATATATATATATATATATATATATATATATATATATATATATAT 1071
772 SerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGluLysIle 791

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US 07-708-962-1

Alignment Scores:

Prod. No.: 4,870-63 Length: 2808
 Score: 726.50 Matches: 236
 Percent Similarity: 36.99% Conservative: 121
 Best Local Similarity: 24.46% Mismatches: 251
 Query Match: 16.16% Indels: 357
 DB: 1 Gaps: 28

US 09-026-459a-49 (1-871) x US 07-708-962-1 (1-2808)

QY 151 LeuLeuLysLysTyrAspValLeuPheAla----LeuPheSer----- 163
 DB 4 AIAIICAAAAAIAICAGGCAATITITITAGATATATITCAAAATCCCAIATGAGAACCA 63
 QY 164 ---LysLeuGluArqThrCysGluLeuLeuTyrLeuThrGluProSerSerSerLeuSer 182
 DB 64 GCAAGATTACAGA-----ASPTGGAGAGCAAGAGAGAGATTGTT 102
 QY 183 ThrGluLeuAsnSerAlaLeuValLeuLysValSerTyrPheThrPheLeuGluAlaLys 202
 DB 103 ICGAGGIIAAGCAI-----CIGIIIAATITCIGTGGACACTTITITCTTAACTAAG 156
 QY 203 GlyLeuValLeuGluMetGluAspSerLeuValIleSerPheGluLeuMetLeuCysVal 222
 DB 157 GGAATITTCGAGATGATGGGACACTTAGAAACCTTATCATTTTACTTCTATGCTGC 216
 QY 223 ICG----- 223
 DB 217 TIGGATCTGATTTTGGCAATGGATTATGAGAGAAATAGACAGACITPRTAATCCCA 276
 QY 224 -----AsPTyrPheIleLysLeuSerPro 231
 DB 277 ICATITAAAGCTTTACCAITGATTTTCATCTGCTGCACTTTACGGCTTCTCCAGAGCCA 336
 QY 232 ProMetLeu----- 234
 DB 337 CCCIGCAICATIGCTGTCACITCTGCACTGCAIGAGGACITCTCGTAGAACCAAAAGCA 396
 QY 245 LeuLysGluProLys-----LysThrGlySer 243
 DB 697 ATAAGAGACACTACTITTAAGATATATITCAAAACITTTTGACAGAGAGATATTAAGA 456
 QY 244 AsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValIleAsnLeuSerLysArg 263
 DB 457 GGCAAAIGCCCTCCGACCTTTCAGCTTTTACGTGATATAGCAAGCACTGAATTAAGAG 516
 QY 264 TyrThrGluThrTyrLeuLysAsnLysAspLeuAspAlaArqLeuPheLeuAspHisAsp 283
 DB 517 IATCAACAGIATGCTTCAACGCTGATTTGATGAGATTTGACAGACGACITCTTIG----- 567
 QY 284 LysThrLeuGluThrAspSerIleAspSerPheGluThrGluThrGluThrProArgLys---- 302
 DB 566 -----GAGAGCAAGCAAG 609
 QY 303 -----SerAsnLeuAspGluGluValAsnVal-----IlePro 313
 DB 610 ACIGIICATACCTCCATTAAGAGAACATACAGACAGACATTAATGTGACATATAACTTICAA 669
 QY 314 PheHis----- 315
 DB 670 CAGTACTTTCGAAAAAAGGCTATTTGCACCTTCTACCCACTCCACCGGAGGAGATAT 729
 QY 316 -----ThrProValArgThrValMetAsnThrIleGluGln 327
 DB 730 ITAGAGAAAAAGAGCAATGATTAATCTGTTTATATAGAGAGAGAGAGAGAGAGAGAGAG 789
 QY 328 LeuMetMetIleLeuAsnSerAlaSerAspGluProSerGluAsnLeuIleSerTyrPhe 347
 DB 790 ITACAGATATIGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849
 QY 348 AsnAsnTyrThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyr 367

DB 850 GAATCTTGCTGGTAAATCTCTGAAAAATATATCAAAAACIAAAGAGAAATAGAGAG 909
 QY 368 ILePheLysGluLysPheAlaLysAlaValGlyGln-----ClyCysValGluIle 384
 DB 910 ACTTTCGTCACACTATATCAATACAGAGAACAGAGAGATCTCAATATAGATTT 969
 QY 385 GlySerGluArqThrLysLeuGlyValArqLeuTyrTyrArqValMetGluSerMetLeu 404
 DB 970 GTCGAAACAGACTAAAGCTGACACAAATTTTGTATTAATAAAATACACACATCTAATC 1029
 QY 405 LysSerGluGluGluArqLeuSerIleGluAsnSerPheLysLeuLeuAsnAspAsnIle 424
 DB 1030 GTTATGAGAAATACAGAAATATGATGAAATGACATGACATGCTTIIAAGAGAGATATA 1089
 QY 425 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSer 444
 DB 1090 TTTATGCTGTTTCTTAAGCTTTTGTCTTGAATTTGTTGCTTGTCTTGTCTTGTCTTGTCT 1143
 QY 445 ThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheProTyrIleLeuAsnValLeu 464
 DB 1144 -----TCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1179
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 DB 1180 AACTTCGACACACTTTTACTTTTATAGGTATATGAGGTATGAGGTATGAGGTATGAGGTATGAG 1239
 QY 485 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeu 504
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 QY 505 AlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGluSerLysAspArg----- 522
 DB 1306 GCAATGAGTACCACTTCTGATCTGAGTGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1359
 QY 522 ----- 522
 DB 1360 AACTGTGAGAAAT 1419
 QY 522 ----- 522
 DB 1420 GATATCTTCTCTCTGAGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1479
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 DB 1540 GATTAAGTCTCTTATCTGAG 1599
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 DB 1600 AAGAAAAAGCTIATGAGAGAGATCATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1659
 QY 522 ----- 522
 DB 1660 TCAAGCATTTACTGCTGCAAAATCTATCAATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1719
 QY 523 -----GlyLysProThrAspHisLeuGluSerAlaCysProLeuAsn----- 546
 DB 1720 ACAGGCTGAGTAAACAG 1776
 QY 537 -----LeuProLeuGluAsnAsnHisThrAlaAlaAsp 547
 DB 1777 GTAATGATGCTGGAGAGAT 1846
 QY 548 MetTyrLeuSerProVal-----ArgSerProLysLys 558
 DB 1837 AAAGTCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1893
 QY 559 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAla 578

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1894  CACACAAATCTTACAAAGACACAGAGGACAAATCAACAGCA--- 1945
579  PheLeuThrGlnTyrSerLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyr 598
1946  ATAAACACACAAAGAACTGGGTGGCTTACACATATTTTACAGAAAGGCTAT 1989
599  ArgLeuAlaTyrLeuArgLeuAsnThrLeuCysSerLeuArgLeuSerGlnHisProGln 618
1990  CATTTGGTAAGTGTACGCTTACGTGATGTATGCTAATA---CTGATATTTTCAATAGAG 2046
619  LeuGlnHisThrLeuThrLeuPheGlnHisThrLeuGlnHisAsnGlnTyrGlnLeuMet 638
2097  TTAACAAAGAAACATAGACAGAGCTTTTCAATTCATTTACCTTACCTGCTGCTCACTAAAG 2196
639  ArgAspArgHisLeuAspGlnHisLeuMetMetCysSerMetTyrGlyTyrLysValLys 658
2197  AAACACACAGCATTTGGATACATGCTGCTTTTGTGGCTTTTATATATCATGGCAAGGTAACA 2166
659  AsnHisAspGlnLysPheGlnHisThrLeuValThrAlaTyrLysAspLeuProHisAlaVal 678
2197  AAAACAAACAAACATTTTCAAGAAATATGAAAGTATGAAATCATGAGGCAAGGCTAAT 2226
679  GlnGlnThrProTyrArgValLeuLys----- 688
2227  AGTCACGATATAACAGGCTGCTGCTCAAAAGCTATTCACACAGCAAGTGTGGCATATAAT 2286
688  ----- 688
2287  AAAATAATAATGATGATTTTGAATGATAGATTGTGACTTACAGATGCTAC/AAAAACA 2346
689  -----GlnGlnGlnTyrAspSerHisGlnValPheTyrAsn 700
2437  CTTACTGCTTTCATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2406
701  SerValPheMetGlnArgLeuLysThrAsnLeuLeuGlnTyrAlaSerThrArg----- 718
2407  AATAATAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2466
719  -----ProProThrLeuSerProLeuProHisThrProThrLysMetThrProArgSerArg 734
2497  CATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2517
735  PheProSerSerProLeuArgPheProGlyTyrAsnThrTyrThrSerProLeuLys 753
2518  CACACACTACACAGGCTGATTTTCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2562
774  SerProTyrLysLeuSerGlnGlyLeuProThrProThrLysMetThrProArgSerArg 773
2563  TCCGAGACAGAAATGGCTACAGGCTT-----ACACACAGAAAGCCGCT 2604
774  ThrLeuValSerHisGlyThrSerGlnLysPheGlnLysPheGlnLysHisAsnGln 793
2605  CTGTGTACCAATTCATGCAAGC-----GCTTGTACAGAGTTTGAAGATATATCAACAG 2658
794  MetValLysAsnSerAsp-----ArgValLeuLysArgSerAlaGlnGly 808
2659  ATATAGAGCAAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2718
809  SerAsnProLys 813
2719  CAATGCTGCTGCAAA 2744

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RESULT 15

US-09-026-459a-49 (1-871) x US-09-152-721B-1 (1-2808)

Sequence 1, Application US/09152721B

Parent No. 5962415

GENERAL INFORMATION:

APPLICANT: LIVINGSTON, DAVID M.

APPLICANT: EMBL, MARK E.

TITLE OF INVENTION: DNA Encoding p107 Tumor Suppressor and

RELATED POLYPEPTIDES

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

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ADDRESS: CHGATE, HALL & STEWARD
STREET: 54 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2H91
COMPUTER REABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 95/298/152,721B
FILING DATE: 15-Nov-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pasternack Esq., Sam
REGISTRATION NUMBER: 29,576
REFERENCE/PACKET NUMBER: 181411 01101V
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ. ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2808 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYDROPHILIC: No
ANTI-SENSE: No
IMMEDIATE SOURCE:
CLONE: cDNA encoding p107
US-08-152-721B-1

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Alignment Scores:
Prod. No.: 1,560-62 Length: 2808
Score: 721.50 Matches: 245
Percent Similarity: 86.99% Gaps: 121
Best Local Similarity: 24.45% Mismatches: 462
Query Match: 16.05% Indels: 467
DB: 2 Gaps: 28

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US-09-026-459a-49 (1-871) x US-09-152-721B-1 (1-2808)

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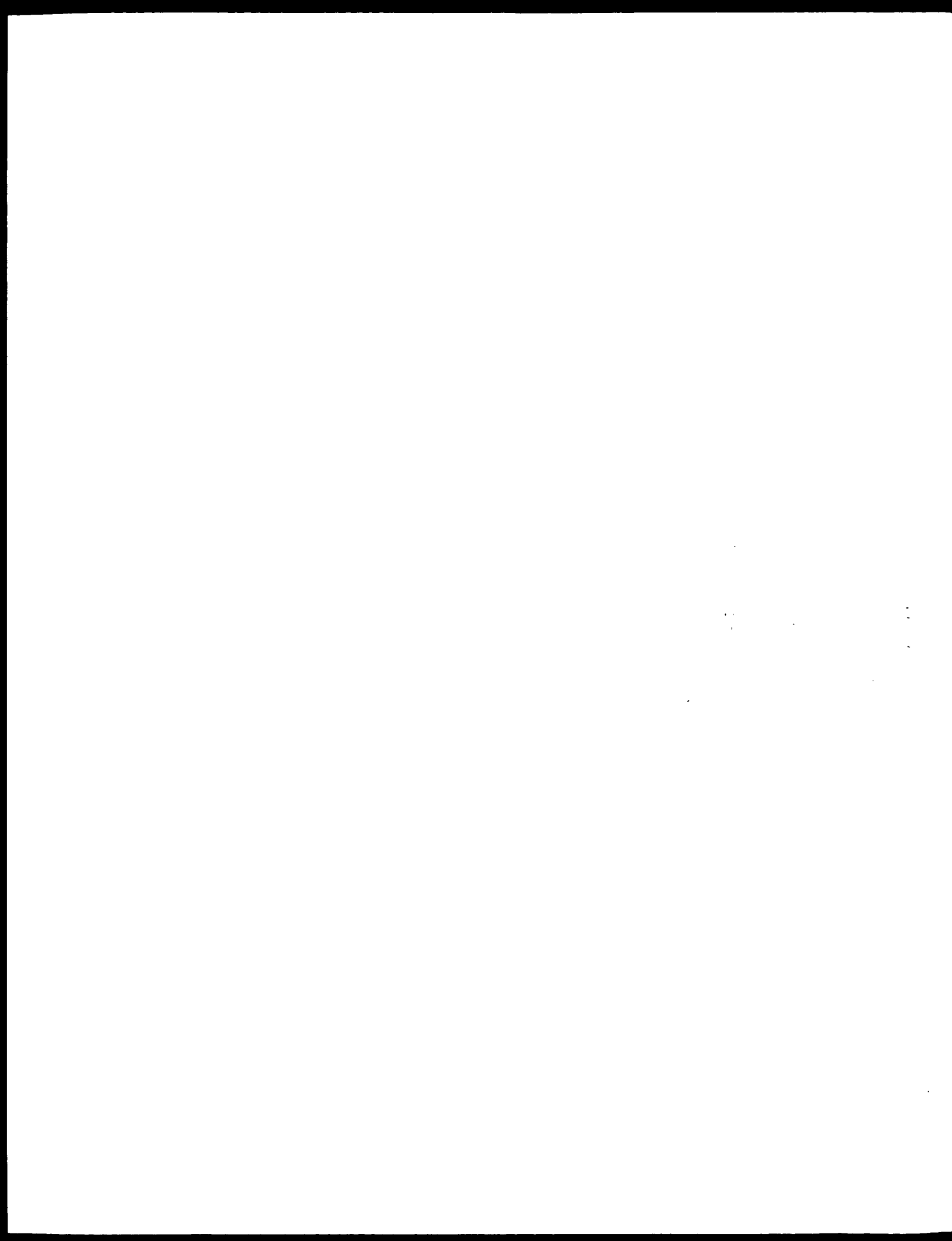
QY 151 LeuLeuLysLysTyrAspValLeuPheAla---LeuPheSer----- 163
DB 4 ATATCAAAAATATGAGCAATTTTTTACATAATTTCAAAATGCAATGCAAGCA 63
QY 164 ---LysLeuGluArgThrCysGlnLeuLeuTyrLeuThrGlnProSerSerHisSer 182
DB 64 CCAAGTTTACAGCA-----AGGAGAGAGAGAGAGAGATTCCT 102
QY 183 ThrGlnHisSerAlaLeuValLeuLysValSerTyrThrThrPheLeuLeuAlaLys 202
DB 103 TGCAGCTGTAAGCAI-----CCTCTTAAATTTCTGTGGACACATTTTGTATATAC 156
QY 203 GlyGlnValLeuGlnMetGlnAspSerValHisSerPheGlnHisMetLeuLysVal 222
DB 157 GGTAAATTTGGATCATTTGGGAGATGACATTAAGAAAGCTTATATATATATAT 216
QY 223 Leu----- 223
DB 217 TTGATCTGATTTTGTGCAATGATATATGTGTCANATATACAAAGACTTGTAAATTA 276
QY 224 -----AspTyrPheTyrLysLeuSerPro 241
DB 277 TCAATTAAGAGTTTACCACTGATTTTCAATCTGACATTTTACGCTTCTTACAGAGCA 446
QY 232 ProMetLeu----- 244
DB 337 CCTGGCATCATCTGCTGATCTGTCGAGAACCTGATGATGATGATGATGATGATGATG 496

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146 2462 CATAAGAGAGAGGCTCCACCAATCTCTCCCTTTCTCACAATAAACAACACAG ..... 2517
97 745 PheProSerSerProLeuArgTlleProGlyGlyAsnTlleTyrTleSerProLeuLys 753
146 2518 CAAAGTCAACCAACCAATTTCCACACACATCCATTATATT ..... 2562
97 754 SerProGlyLysTleSerGlnGlyLeuProThrProThrLysMetThrProArgSerArg 773
146 2563 TCCAGGACCAAGATGGTCAAGGCTT ..... ACACCAAGACGGCT 2604
97 774 TleLeuValSerTlleGlyGlySerPheGlyThrSerGlnLysPheGlnLysTlleAsnGln 793
146 2605 CTGCTGACCAAGGTTCAAGGCAAGT ..... CCTTCACAGAGTTTCACCAATATCAACACAC 2658
97 794 MetValCysAsnSerAsp ..... ArgValLeuLysArgSerAlaGlnGly 808
146 2659 ATGATAAAGCAAGCTAGAGACAGCAACCAACCAAGCAAGCAATATAGCAATATGATGCA 2718
97 809 SerAsnProProLys 813
146 2719 GAAATCCCTGGGAAA 2733
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Search completed: January 19, 2003, 05:37:24
Job Time : 162.548 secs




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QY 701 IleAspSerPheThrGlnAspThrProArgLysSerAsnLeuAspGluGluValAsn 220
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QY 721 ValIleProPheHisIleProValArgGluValMetAsnThrIleGlnGlnLeuMetMet 240
DB 772 GTAAATGCTCCACACACACACACACACACACACACACACACACACACACACAC 831
QY 781 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerIyrPheAsnAsnCys 260
DB 842 ATTTTAAATTCAGCAAGGATGATCAACCTTCAGAAATCTGATTTCCCTATTTTAAACAACCTGC 891
QY 861 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
DB 842 ACAGTGAATCCCAAAACAAAGATATACCAAAAGACCTCAAGCATATAGCATACATCTTTAA 951
QY 881 GluLysPheAlaLysAlaValGlyGlyGlyCysValGlyIleGlySerGlnArgTyrLys 300
DB 962 CAGAAATTTCTTAAGGATGTAAGGATGTAAGGATGTAAGGATGTAAGGATGTAAG 1011
QY 981 LeuGlyValArgGluValArgValMetGluSerMetLeuLysSerGluGluGluArg 320
DB 1012 CTTCAGACATTCCTGATATACAGGAGTAAGTGAATGCTTAAATCAAGACAGACAGCA 1071
QY 1021 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu 340
DB 1072 TATCCATTCACAAATTTTAGCAAACTCTTCGAATCACAACATTTTTCATATGCTCTTAA 1131
QY 1081 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerIleGluAsnLeuAsp 360
DB 1142 GGTGATGCTCTTGAATTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1191
QY 1161 SerGlyThrAspLeuSerPheProThrIleLeuAsnValIleuAsnLeuLysAlaPheAsp 380
DB 1142 CTTCGAAACAGATTTCTCTCCCATGCAATCTGCAATGCTGCTTAAATTTAAAGCCTTTGAT 1251
QY 1181 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
DB 1252 TTTTACAAAGTGAATGAAAGCTTTTATGAAAGCAGCAAGCAAGCAAGCAAGCAAG 1311
QY 1201 LysHisLeuGluArgCysGluHisArgIleMetGlnSerLeuAlaThrLeuSerAspSer 420
DB 1312 AAATATTATTAACATGTAACATGTAACATGTAACATGTAACATGTAACATGTAACAT 1371
QY 1221 ProLeuPheAspGluIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGlu 440
DB 1372 GCTTATTTGATCTTATTAACAAATCAAGGACCGACGACGACCAACCTGATCACCCTTGA 1431
QY 1241 SerAlaLysPheGluAsnLeuPheGluGluAsnLeuIleThrAlaAlaAspMetTyrLeu 460
DB 1412 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1491
QY 1261 SerProValArgSerProLysLysLysCysThrThrThrArgValAsnSerThrAlaAsn 480
DB 1442 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1551
QY 1281 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
DB 1512 GCACACACACACACACACACCTCAGCTTCCACACCCACAGCCATGAAATCTACCTCTCT 1611
QY 1301 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGlyGlu 520
DB 1612 TCACAGTCTTATAAAAGCTGATGCTACCTACCTACCTACCTACCTACCTACCTACCT 1671
QY 1321 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrPheLeuPheGluHisThr 540
DB 1672 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1731
QY 1341 LeuGluAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
DB 1742 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1791
QY 1361 MetTyrGlyIleGlyValLysAsnIleAspLeuLysPheLysIleValThrAla 580

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DB 1792 ATGTATGCTATATCAAGTCAACATATATATATATATATATATATATATATATATAT 1851
QY 581 TyrLysAspLeuProHisAlaValGlnGlnThrPheLysArgValLeuIleLysGluGlu 600
DB 1852 TAAAGGATCTTCTTAAAGGATCTTCTTAAAGGATCTTCTTAAAGGATCTTCTTAAAGG 1911
QY 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
DB 1912 GAGTATCATCTCTATATATATATATATATATATATATATATATATATATATATATAT 1971
QY 621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
DB 1972 ATTTTGCATATATCTTCAACAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2031
QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyClyAsnIleLysIleSer 660
DB 2032 AGCTCTTAAATTTCTTAAATTTCTTAAATTTCTTAAATTTCTTAAATTTCTTAAAT 2091
QY 661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
DB 2092 CCGCTGACAGCTCTATATAAAATTCAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCT 2151
QY 681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
DB 2152 AGATCAAGATTTATATATATATATATATATATATATATATATATATATATATAT 2211
QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
DB 2212 ATAAATAGATATATATATATATATATATATATATATATATATATATATATATAT 2271
QY 721 ProProLysPheGluLysLysLeuArgPheAspIleGlyLysSerAspGluAlaAspGly 740
DB 2272 CTTCTTAAATCACTGAAATCACTGAAATCACTGAAATCACTGAAATCACTGAAATCA 2331
QY 741 SerLysIleLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 760
DB 2332 AGTAAATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2391
QY 761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
DB 2392 GCTAAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2451
QY 781 Lys 781
DB 2452 AAA 2454

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RESULT 3
US-09-459-522-34
: Sequence 34, Application US/09469522
: Patent No. US29020151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
:             Hu, Shi-Xue
:             Benedict, William F.
:             Zhou, Yunli
: TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
:                     PROTEINS
: NUMBER OF SHOWNCHRS: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Aruold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09,469,522

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1 CURRENT APPLICATION DATA:
2
3   APPLICATION NUMBER: US/09/469,522
4   FILING DATE: 22-Dec-1999
5   CLASSIFICATION: unknown
6
7   PRIOR APPLICATION DATA:
8
9     APPLICATION NUMBER: 09/026,459
10    FILING DATE: unknown
11
12   ATTORNEY AGENT INFORMATION:
13
14     NAME: Hibler, David W.
15     REGISTRATION NUMBER: 41,071
16     REFERENCE/DOCKET NUMBER: UTXC:506
17
18   TELECOMMUNICATION INFORMATION:
19
20     TELEPHONE: 512/418-3000
21     TELEFAX: 512/474-7577
22
23   INFORMATION FOR SEQ ID NO: 38:
24
25     SEQUENCE CHARACTERISTICS:
26
27       LENGTH: 3323 base pairs
28       TYPE: nucleic acid
29       STRANDEDNESS: single
30       TOPOLOGY: linear
31
32     FEATURE:
33
34       NAME/KEY: CDS
35       LOCATION: 7..2559
36       SEQUENCE DESCRIPTION: SEQ ID NO: 38:
37
38   US-09-469,522-38

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541 LeuGlnAsnGlyTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 560
1469 CTTCAAAACACATCAACAAATATGACACACAGCATTTGGACCAAAATATCATGTCTTCC 2028
561 MetGlyTyrGlyCysValLysAsnIleAspLeuLysPheLysIleValThrAla 580
2029 ATTATGATATATATGAAAT 2088
581 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
2089 TACAAGAGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2148
601 GluTyrAspSerIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
2149 GACTATCATCTTAT 2208
621 PheLeuGlyTyrAlaSerThrArgProThrProThrLeuSerProGlnIleProHisIleProArg 640
2209 ATTTCAGATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2268
641 SerProLysPhePheSerProLeuArgIleProGlyCysIleTyrIleSer 660
2269 ACCCTTACAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2328
661 ProLeuLysSerProTyrLysIleSerGluLysLeuProThrProThrLysMetThrPro 680
2329 CTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2388
681 ArgSerArgIleAlaValSerIleGlyCysSerPheGlyThrSerGluLysPheGluLys 700
2389 AGATCAAGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2448
701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluCysSerAsn 720
2449 ATAAATCATATGAT 2508
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2509 CTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2568
741 SerLysHisLeuProGlyCysLysSerPheGlnGlnLysLeuAlaGluMetThrSerThr 760
2569 AGTAACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2628
761 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 780
2629 CCAACACCAATCAAAAGCAGAAATGAATGATGATGATGATGATGATGATGATGATGATG 2688
781 Lys 781
111
2689 AAA 2691

RESULTS

US-09-469-522-40

Sequence 40, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F

Zhou, Yunli

TITLE OF INVENTION: MODIFIED PETINOBLASTIN-TYPE SUPPRESSOR

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

STREET: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER FEATABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: ITXC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 3461 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2697
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-469-522-40

Alignment Scores:

Score: 0 Length: 3461
Percent Similarity: 4017.00 Matches: 781
Best Local Similarity: 100.00% Conservatives: 0
Query Match: 100.00% Mismatches: 0
DB: 10 Indels: 0
Gaps: 0

US-09-026-459A-37 (1-781) x US-09-469-522-40 (1-3461)

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Db 355 ATGTCAGACCTTTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 414
QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerIleSerThrGluIleAsnSer 40
Db 415 ACATCTGAACCTATATATTTGACACACCCAGCAGTTCGATATCTACTGAAATAATTC 474
QY 41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
Db 475 GCATTGGTGCTAAAGATTTCTTGATCACAATTTTATTAGCTAAAGAGAGATATACAA 534
QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
Db 535 ATGTAAGAT 594
QY 81 LysLeuSerProMetLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
Db 595 AAAATCTCAACCTCAGATGCTTCAAGAGACATATAAAGAGCTGTATACCACTAAAT 654
QY 101 GlySerProArgThrProArgGlyGlyAsnArgSerAlaArgIleAlaLysGluLeu 120
Db 655 GATTAT 714
QY 121 GluAsnAspThrArgIleGlnValLeuCysLysGluHisGluCysAsnIleAspGlu 140
Db 715 GAAATGATACAAAGATATTTGAAGTTCTCTGTAAAGAAATGAAATGTAATATATAG 774
QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
Db 775 GTGAAATATGTTTATTTCAAAATTTTATACCTTTTATGAATTTCTTGGACTTGTAA 834
QY 161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
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1b 2008 CCGTTCGCTGCTGAGACAGCAAAATAGAACATAIACATGCAACCCCTTTTCAGACACACC 2067
 QY 541 LeuAlaAsnGluTyrGluLeuMetArgAspArgHisLeuAspGluLeuMetMetCysSer 560
 1b 2068 CTGAGAAATAGTATGAAATCAATGAGACAGACAGCATTTGACAGCAAAATATATGCTGTCC 2127
 QY 561 MetTyrGlyLeuCysLysValLysAsnLeuAspLeuLysPheLysIleLeuValThrAla 580
 1b 2128 ATGATATGATATGAAATGAAATATAGAACTTAAATTCAAAATCATTTGTAACAGCA 2187
 QY 581 TyrLysAspLeuProHisAlaValIleLeuThrPheLysArgValLeuIleLysGluGln 600
 1b 2188 TAAAGCACTGCTGCAAGTGTTCAGGACAGACATTCAAACGGTGTTCATCAAAAGAACAG 2247
 QY 601 GluTyrAspSerIleLeuValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
 1b 2248 GATATGATCTCTATATATGATATGATATGATATGATATGATATGATATGATATGATATG 2307
 QY 621 ILeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
 1b 2308 ATTTCAGATATGCTTTCAGACAGAGCGGCTATCTTCACCAAAATACACATTCGTCGA 2367
 QY 641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
 1b 2368 AGTCTCTATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 2427
 QY 661 ProLeuLysSerProTyrLysIleSerGluLysLeuProThrProThrLysMetThrPro 680
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 QY 681 ArgSerArgIleLeuValSerIleGlyGlySerPheGlyGlySerPheGlyGlySerPhe 700
 1b 2488 AGATCAAGAAATCTAT 2547
 QY 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluLysSerAsn 720
 1b 2548 AAAAAACAGATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2607
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 1b 2728 GAAACATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 2787
 QY 781 Lys 781
 1b 2788 AAA 2740
 RESULT 10
 US 09 469 522 1
 Sequence 1: Application US/09/469522
 Patent No. US2002015146A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Shi Xue
 Hu, Shi Xue
 Zhou, Yuhui
 BENEDICT, William F.
 TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 PROTEINS
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Burke
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210 4433

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.40
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/469,522
 FILING DATE: 22-Dec-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTX:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3555 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2790
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-469-522-1

Alignment Scores:
 Pred. No.: 0 Length: 4555
 Score: 4017.00 Matches: 781
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-026-459a-37 (1-781) x US-09-469-522-1 (1-3555)

QY 1 MetSerArgLeuLeuLysLysLysLysValLeuPheAlaLeuPheSerLysLeuThrArg 20
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 QY 21 ThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer 40
 1b 508 ACATGTCAACTTATATATTGACACAAACCCAGCAGTTCATATCTGATATCTGATATCT 567
 QY 41 AlaLeuValLeuLysValSerIleThrPheLeuLeuAlaLysGlyLeuValLeuGln 60
 1b 568 GCATTGTGTATAAAGTTTCTGATCAATTTTATATATATATATATATATATATATATAT 627
 QY 61 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuLysValLeuAspLysPheIle 80
 1b 628 ATGCAAGCAATCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 687
 QY 81 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
 1b 688 AAACCTCCACCTGCGCACTGTGTGTCAAAGAACCAATATAAAACATGTGTATATAATAT 747
 QY 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu 120
 1b 748 GATTCATCTCGAATACCAAG 807
 QY 121 GluAsnAspThrArgIleIleGluValLeuCysLysGlnHisSerLysCysAsnIleAspGln 140
 1b 808 GAAAAATGATCAACAAGAAATATGCAAGTCTCTGTAAGCAAAATGCAAAATGCAAAATG 867
 QY 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 160
 1b 868 GTGAAAAATGTTTATTTTCAAAAAATTTTATACCTTTTATGAAATCTCTCTGTAATTT 927

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161 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 180
162 TCTAATGACATTCAGAGGTTGAAATCTTTCAACCATACAGAGAAATTTATCTTAA 987
163 AsnLysAspLeuAspAlaArgLeuPheLeuAspLysAspLysThrLeuGlnThrAspSer 200
164 AATAAGATCTAGATGCAAGATTAATTTTGATCATCATCAAAATCTCTTCACTCATCT 1047
165 IleAspSerPheGluThrGluAlaArgProArgLysSerAspLeuAspGluGluValAsn 220
166 ATATATATTTTGAACATATGAAATCTTCAAAAGATTAACCTTGAAGAGAGAGTGAAT 1107
167 ValIleProProHisThrProValArgThrValMetAsnThrIleGluGlnLeuMetMet 240
168 GTAAATTTCTCCATATAGTCAATATAGGAGCTTTATGAGACATTTATGACATATAT 1167
169 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 260
170 ATTTTAAATTCATCAAGTCAATCACTTTCAGAAATCTGATTTCTATTTTAACTGTC 1227
171 ThrValAspProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280
172 AATGTAATCCAAAGAAAGTATATCTGAAAGAGTGAAGATATAGGATACATCTTTAA 1287
173 GluLysPheAlaLysValValIleGlyCysValGluIleGlySerGlnArgTyrLys 300
174 GATAATTTTCTAAAGTGTGAGATATGAGTTTGTGAAATTTGATGATCAATGATCAAA 1347
175 LeuLysValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluLysArg 320
176 CTGTGAGTGTGATATATGAGTAAATGGAATGCAATGTAATCAAGAGAAAGACGA 1407
177 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheIleHisMetSerLeuLeu 340
178 TTATGCAATTCAAATTTTAACTTCGAAATGATGACAAATTTTTCATATGCTCTTAT 1467
179 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 360
180 GTGTGAGTGTGATATATGAGTAAATGGAATGCAATGTAATCAAGAGAAAGACGA 1527
181 SerGlyThrAspLeuSerPheProIleLeuAsnValLeuAsnLeuLysAlaPheAsp 380
182 TCTGGAACACATTTGCTTTCCTCCATGATCTGATCTGCTTAATTTTAAAGCTTTGAT 1587
183 PheTyrLysValIleGluSerPheIleLysAlaGluLysAsnLeuThrArgGluMetIle 400
184 TTTTAAAGATGATGAAATCTTTTATCAAGATGAAAGTAACTTGTGATGATGATGATA 1647
185 LysAspLeuGluArgCysSerHisArgIleMetGluSerLeuAlaThrLeuSerAspSer 420
186 AATATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1707
187 ProLeuPheAspLeuIleLysGlnSerLysAspArgGluLysProThrAspHisLeuGlu 440
188 CCLTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1767
189 SerAlaLysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetIleLeu 460
190 TCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1827
191 SerPheValArgSerProLysLysCysGlySerThrThrArgValAsnSerThrAlaAsn 480
192 TCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1887
193 AlaGluThrGlnAlaThrSerAlaPheGluThrGluLysProLeuLysSerThrSerLeu 500
194 GAGAGACATATATATATATATATATATATATATATATATATATATATATATATATAT 1947
195 SerLeuPheTyrLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuLysGlu 520
196 TCACTGTTTTTATATATATATATATATATATATATATATATATATATATATATATATAT 2007
197 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleThrThrLeuPheGluHisThr 540

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2008 CCGCTCTCTCTGAGATCCCAACAAATACAAATATATCATCATGACCCCTTCCACACATCC 2067
541 LeuGlnAsnGluTyrGluLeuMetArgAspAluHisLeuAspGlnIleMetMetCysSer 560
2068 CTTCCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2127
561 MetTyrGlyIleCysLysValIleLysAsnIleAspLeuLysPheCysIleIleValIleAla 580
2128 ATGTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2187
581 TyrLysAspLeuProHisAlaValIleGlnIleThrPheLysArgValIleLysGluGlu 600
2188 TACAAGATATATATATATATATATATATATATATATATATATATATATATATATATAT 2247
601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
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641 SerProLysPheProSerProIleGluArgIleThrGlyCysAsnIleIleIleSer 660
2368 ACCCTTACAGTTTCTAGTTCACCTTACGAAATCTGAGAGGAAACATATATATATATAT 2427
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2488 ACATCAAAATCTTATATATATATATATATATATATATATATATATATATATATATATAT 2547
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721 ProProLysPheLeuLysLysLeuArgPheAspIleGluGlySerAspGlyValAspGly 740
2608 CCGCTTAAACCATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAAT 2667
741 SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerHis 760
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781 Lys 781
2788 AAA 2790

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RESULT 11

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US-09-454-531-143
: Sequence 143, Application US/09454531
: Patent No. US20020155180A1
: GENERAL INFORMATION:
: APPLICANT: Watson, 200
: TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
: FILE NUMBER: 680290-77
: CURRENT APPLICATION NUMBER: US/09454531
: PRIOR APPLICATION NUMBER: US/09454531
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: US/09454531
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: US/09454531
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: US/09454531

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D6	1300	AATTAATAACAAAGGACACAACTCCACAAAATCGATTCCTATTAACCACTGCC	1359
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D6			
D6	1360	ATAGTGAAATCAAAAAGAAGATATAATGAAAACTTGAAGSATATAGATATCATCTTTAAA	1419
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D6	1480	CTTAGACATGGTTCGATATATACGATAAATGCAATTCGCTTAATTCAGAGCAAGAACCA	1539
Q7	321	LeuSorThleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeu	340
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D6			
D6	1660	TTTGAAATAGATTTGCTCTCTCAAGCATGCAATTCGAAATGCTTAATTAAGAAGCTTTGAT	1719
Q7	381	PheTytyLysValIleGlnSorPheIleLysAlaGluGlyAsnLeuIthrArqGluMetIle	400
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D6	1720	TTTTNAAAGTGATGAAAGTTTATCAAACAGANAGCACTTGATCANAGAAATGATA	1779
Q7	401	LysHisLeuGlnArqCysGluHisArqIleMetGluSerLeuAlaTripleuSorAspSer	420
D6			
D6	1780	AAATATTTAGAACATGATCAAAATCGAAATCGAAATCGCAATCGCTGCAATCGCTCAGATTC	1839
Q7	421	ProGluPheAspLeuIleLysGluSerLysAspArqGluGlyProThrAspHisLeuGlu	440
D6			
D6	1840	CTTTATTTGATCTTTAAATAAACAAAGCAACACAGAGCATAACATGACCTTCGAA	1899
Q7	441	SerAlaCysProLeuAsnGlnProLysGlnAsnAsnIsthrAlaAlaAspMetTytyLeu	460
D6			
D6	1900	TTGGTTGGCTCTTAATCTCTCTCTGAGAAATATACATGACATGACAGATATGATCTT	1959
Q7	461	SerProvalArqSorProLysLysCysGlySerIthrThrArqValAsnSorIthrAlaAsn	480
D6			
D6	1960	CTCTGCTAACTATCTCAAAACAAAAGCTTCACATGGCTGGTGAATTCATCGCCAAT	2019
Q7	481	AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSorThrSerLeu	500
D6			
D6	2020	CTAGACATCAAACTAACTCACTCTCCAGATCCAGAGGCTATTCGAAATCTAGCTCTCTT	2079
Q7	501	SerLeuPheTytyLysValItyrArqLeuAlaTytyLeuArqLeuAsnIthrLeuCysGlu	520
D6			
D6	2080	TACTGTTTTATMAAAAGTGATGGGTAGCTATCTCCGGCTAAATATACITITGTGAA	2139
Q7	521	ArqLeuLeuSerGluHisSpreGlnLeuHisIleIleThrPthrLeuPheGlnHisThr	540
D6			
D6	2140	CAGCTCTCTCTCGACATCAAAATAGAAATATATCATCTCGAATCTTCCAGCACACC	2199
Q7	541	LeuGlnAsnGlnTytyGluGluMetArqAspArqHisLeuaspGlnIleMetMetCysSer	560
D6			
D6	2200	CTGACAAATGAGATATCAAAATCATACAGACACAGCAATTCGACATAATCATCTGTCC	2259
Q7	561	MetTytyTytyLeuCysValLysAsnIleAspLeuLysPheCysIleIleValThrAla	580
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Q7	581	TytyAspLeuprofHisAlaValGlnGlnIthrPheLysArqValIleouIleLysGluGlu	600
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Sequence 46, Application US/09469522
Patent No. US2002015461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210 4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22 Dec 1999
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: Hilber, David W.
REGISTRATION NUMBER: 41,071

REFERENCE/DEPOSIT NUMBER: UTXC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEX: 512/474 7577
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2613
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File: us-09-026-459a-36

RefSeq score: 4114

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Gapop: 10.0, Gapext: 1.0

Searched: 49868 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 78776

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database: Published Applications, NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4114	100.0	3113	10	US 09 469-522-36 Sequence 36, Appl
2	4107	99.8	3218	10	US 09 469-522-36 Sequence 3, Appl
3	4107	99.8	3266	10	US 09 469-522-36 Sequence 34, Appl
4	4107	99.8	3423	10	US 09 469-522-36 Sequence 32, Appl
5	4107	99.8	3423	10	US 09 469-522-36 Sequence 38, Appl
6	4107	99.8	3492	10	US 09 469-522-36 Sequence 30, Appl
7	4107	99.8	3455	10	US 09 469-522-36 Sequence 28, Appl
8	4107	99.8	3461	10	US 09 469-522-36 Sequence 40, Appl
9	4107	99.8	3554	10	US 09 469-522-36 Sequence 50, Appl
10	4107	99.8	3555	10	US 09 469-522-36 Sequence 1, Appl
11	4107	99.8	4839	9	US 09 964-842A-296 Sequence 143, App
12	4096	96.5	3447	10	US 09 469-522-36 Sequence 42, Appl
13	2627.4	90.8	3161	10	US 09 469-522-42 Sequence 44, Appl
14	2525	90.7	3377	10	US 09 469-522-46 Sequence 46, Appl
15	2748.6	88.3	3383	10	US 09 469-522-48 Sequence 48, Appl
16	2410.4	77.4	2995	10	US 09 860-211-77 Sequence 7, Appl
17	428	13.7	451	9	US 09 796-692-7740 Sequence 7740, Ap
18	142.2	4.6	411	10	US 09 864 761-4131 Sequence 3131, Ap
19	129	4.1	129	10	US 09 864 761 19910 Sequence 19910, A

ALIGNMENTS

RESULT 1

US 09-469-522-36

Sequence 36, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Hendrick, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED REINDEBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER of SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522

FILING DATE: 22-Dec-1999

CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: Hilbert, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTX:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-1000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 3113 base pairs

TYPE: nucleic acid

Sequence 296, Appl
Sequence 47, Appl
Sequence 2546, Ap
Sequence 1, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 42, App
Sequence 44, App
Sequence 4, Appl
Sequence 11218, A
Sequence 34521, A
Sequence 4582, Ap
Sequence 154, App
Sequence 5558, Ap
Sequence 31244, A
Sequence 5785, Ap
Sequence 1, Appl
Sequence 12358, A
Sequence 2769, Ap
Sequence 4147, Ap
Sequence 4050, Ap
Sequence 749, App
Sequence 5166, Ap
Sequence 4, Appl

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: Arnold, White & Durkin
 3 STREET: P.O. Box 4434
 4 CITY: Houston
 5 STATE: TX
 6 COUNTRY: USA
 7 ZIP: 77210 4434
 8
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: Floppy disk
 11 COMPUTER: IBM PC compatible
 12 OPERATING SYSTEM: PC-DOS/MS-DOS
 13 SOFTWARE: Patent In Release #1.0, Version #1.0
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 15 CURRENT APPLICATION DATA:
 16 APPLICATION NUMBER: US/09/459,459
 17 FILING DATE: 22 Dec 1999
 18 CLASSIFICATION: Unknown
 19 PRIOR APPLICATION DATA:
 20 APPLICATION NUMBER: 09/026,459
 21 FILING DATE: Unknown
 22
 23 ATTORNEY/AGENT INFORMATION:
 24 NAME: Hubert, David W.
 25 REGISTRATION NUMBER: 41,071
 26 REFERENCE/DOCKET NUMBER: OLC:506
 27 TELECOMMUNICATION INFORMATION:
 28 TELEPHONE: 512/418 4000
 29 TELEFAX: 512/414 7577
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 31 INFORMATION FOR SEQ ID NO: 48:
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 3423 base pairs
 34 TYPE: nucleic acid
 35 STRANDEDNESS: single
 36 TOPOLOGY: linear
 37
 38 NAME/KEY: CDS
 39 LOCATION: 7..2559
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 41 SEQUENCE DESCRIPTION: SEQ ID NO: 38:
 42 US 09 459 522 48

Query Match 99.8% Score 3107; DH 10; Length 3323;
 Best local similarity 100.0%; Pred. No. 0;
 Matches 3107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
US-09-469-522-28
Sequence 28, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1 0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-469-522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTXC-506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 3455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2691
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-469-522-28
Query Match 99.8%; Score 4107; DB 10; Length 4455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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2472	AACTAAGAACACCTTTACAAAATTTGTTGCTATCTATCTATCTCCAAATGCAATTTGATGCTG	3266
2473	AACTAAGAACACCTTTACAAAATTTGTTGCTATCTATCTATCTCCAAATGCAATTTGATGCTG	3286
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2486	AACTAAGAACACCTTTACAAAATTTGTTGCTATCTATCTATCTCCAAATGCAATTTGATGCTG	3546
2487	AACTAAGAACACCTTTACAAAATTTGTTGCTATCTATCTATCTCCAAATGCAATTTGATGCTG	3566
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2492	AACTAAGAACACCTTTACAAAATTTGTTGCTATCTATCTATCTCCAAATGCAATTTGATGCTG	3666
2493	AACTAAGAACACCTTTACAAAATTTGTTGCTATCTATCTATCTCCAAATGCAATTTGATGCTG	3686
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 $\frac{1}{\sqrt{\pi}}$

1000

US 2003/0419,322 A1
 : September 40, Application US/09469522

Report No. HS-20020151461A1

GENERAL INFORMATION:

APPLICANT: XU, HONG-JI

$$\frac{1}{f} = \frac{1}{f_1} + \frac{1}{f_2} + \frac{1}{f_3} + \dots$$

Benedict, W.

Zhou Yundj; DELEGATE, WITNESS

THE F. W. WYLLIE CO. LTD.

THE STATE OF INNOVATION. PROFILE AND PROSPECTS

NUMBER OF SEQUENCES: 51 PROTEINS

NUMBER OF SEQUENCES: 1
ADDRESS INDEPENDENT ADDRESS

CORRESPONDENCE ADDRESS: ADDRESS: APPROX. WEIGHT:

ADDRESSEE: AMHORG, WHITE
STREET, D O BOX 4433

STREET: P.O. BOX 4433
CITY: Houston

CITY: HOUSTON

[illegible]

LIBRARY: USA
350-2710-433

ZIP: 77210-4433
COMPUTING CENTER FOR SCIENCE

COMPUTER READABLE FORM.

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; MEDIUM TYPE: Floppy disk
;

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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS,

; SOFTWARE: Patent In Releas

NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESS: Artold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Pat-in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 09/469,422
 FILING DATE: 22-Dec-1999
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/326,459
 FILING DATE: Unknown
 ATTORNEY/AGENT INFORMATION:
 NAME: Biblet, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTXC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3555 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2790
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 99.8%; Score 3107; DB 10; Length 3555;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	606	AATGAGACTTATATATTTGACACAAAGAGAGTGGATATCTATGAAATATAATCT	567
49	127	GAATTCGCTTAAAGAGTCTTGGACACATTTTATTAAGCGGAGAGATTAACA	186
DB	608	GAATTCGCTTAAAGAGTCTTGGACACATTTTATTAAGCGGAGAGATTAACA	627
49	167	ATGGAAGATGATCTGATTCATTTTCGTTAATGATGATGCTGCTGATATTTAT	246
DB	628	ATGGAAGATGATCTGATTCATTTTCGTTAATGATGATGCTGCTGATATTTAT	687
49	247	AAAGCTTACGCTGGATGCTTGTCAAGAGACATATAAAGAGCTGTATACCCATTA	306
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49	667	GTAAATCTCCACACACACACACACCTTAGGACTCTGATGAACTATGCAACATTA	726
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DB	1228	ATAGTGAATCTTGAACACACAGACACACGAAAGATTAACCTTGAAGAGTGA	1287
49	847	GAGAAATTTGCTTAAAGCTTGGGACACAGCTTGGGCTGCTGCTGCTGCTGCTG	906
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49	907	TTTGAATCTGCTTGAATTAATGAGATTAATGATGATGATGATGATGATGATG	966
DB	1348	TTTGAATCTGCTTGAATTAATGAGATTAATGATGATGATGATGATGATGATG	1407
49	967	TTTGAATCTGCTTGAATTAATGAGATTAATGATGATGATGATGATGATGATG	1026
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DB	1528	TCTGAGACAGATTTGCTTTCCCATGATGATGATGATGATGATGATGATGATG	1587
49	1147	TTTTCAAACTTCATGCAAGATTTTCAAGACACAGAGGAGTGAACAGAGAAATCA	1206
DB	1588	TTTTCAAACTTCATGCAAGATTTTCAAGACACAGAGGAGTGAACAGAGAAATCA	1267
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QY	2467	CTTTTCTGGATATAAAATGTGCATGCGCAATCTGTTGGGNGATGCTCAAGCCACATTTGAA	2526
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QY	2887	AAAAATATTAATTTTACACATTTATTTTATTTATTTATTTGAAATCTGATATACTGCTGT	2946
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QY	2947	GGTTGGTTTTATAAAATTTTGTCTTTTAAATATAAAGCTGGGAATATAAATATAA	3006
DB	3017	GGTTGGTTTTATAAAATTTTGTCTTTTAAATATAAAGCTGGGAATATAAATATAA	3276
QY	3007	TCATATATATATATATCAAAATACATTTCAATCTCAGAAATCAAAAGCAATTTACTGAT	3066
DB	3077	TCATATATATATATATCAAAATACATTTCAATCTCAGAAATCAAAAGCAATTTACTGAT	3336
QY	3067	TATTTCTGATCCCAACTTATGTTTTTAAATGAGGATTTATTTGATGAT	3113
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Job time : 121.044 secs

GenPac version 5.1.1.3
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Run on: January 18, 2003, 04:31:54 : Search time 60.7453 seconds
(without alignments)
6107.852 Million cell updates/sec

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Searched: 93868 seqs, 22744149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum hit seq length: 0
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Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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DB=pubmed Applications NA -GMT-fastap -SUFFIX=pub -MINMATCH=0.1
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MAXLEN=200000000 -SEXP=NS0002459 -COGN=1 -COGN_FUZZ=152139 -23369
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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4278	100.0	4266	10	US-09-469-522-34	Sequence 34, Appl
2	4273	99.9	4424	10	US-09-469-522-42	Sequence 32, Appl
3	4274	99.9	4424	10	US-09-469-522-40	Sequence 30, Appl
4	4273	99.9	4455	10	US-09-469-522-28	Sequence 28, Appl

5	4274	99.9	3555	10	US-09-469-522-1	Sequence 1, Appl
6	4273	99.9	4859	9	US-09-964-541-143	Sequence 143, App
7	4263	99.6	2995	10	US-09-864-211-7	Sequence 7, Appl
8	4263	99.6	3554	10	US-09-469-522-50	Sequence 50, Appl
9	4217	98.6	3423	10	US-09-469-522-48	Sequence 48, Appl
10	4217	98.6	3461	10	US-09-469-522-40	Sequence 40, Appl
11	4192	98.3	3218	10	US-09-469-522-3	Sequence 3, Appl
12	4017	93.9	3113	10	US-09-469-522-46	Sequence 46, Appl
13	3930.5	91.9	3473	10	US-09-469-522-46	Sequence 46, Appl
14	3923.5	91.7	3483	10	US-09-469-522-48	Sequence 48, Appl
15	3877.5	90.6	3447	10	US-09-469-522-42	Sequence 42, Appl
16	3550	83.0	4161	10	US-09-469-522-44	Sequence 44, Appl
17	790	18.5	3960	9	US-09-292-758-37	Sequence 37, Appl
18	516.5	12.1	3747	10	US-09-770-657-1	Sequence 1, Appl
19	516.5	12.1	3747	12	US-10-025-676-2	Sequence 2, Appl
20	355.5	8.3	3299	10	US-09-220-091-4	Sequence 4, Appl
21	243	5.7	411	10	US-09-864-761-141	Sequence 141, Ap
22	238	5.1	129	10	US-09-864-761-19910	Sequence 19910, A
23	177.5	4.1	304	10	US-09-964-824-296	Sequence 296, App
24	151	3.5	5864	10	US-09-864-864-405	Sequence 405, App
25	150	3.5	6773	10	US-09-864-864-436	Sequence 436, App
26	148.5	3.5	3624	9	US-10-108-605-215	Sequence 216, App
27	148.5	3.5	10096	10	US-09-960-253-163	Sequence 163, App
28	146.5	3.4	19169	10	US-09-864-864-292	Sequence 292, App
29	146.5	3.4	10211	10	US-09-964-456-1154	Sequence 1154, Ap
30	146.5	3.4	10211	10	US-09-967-768A-186	Sequence 186, App
31	145.5	3.4	324	9	US-09-796-692-2646	Sequence 2546, Ap
32	141.5	3.3	9274	10	US-09-885-545-3	Sequence 3, Appl
33	141	3.3	4754	10	US-09-982-091A-1	Sequence 1, Appl
34	138.5	3.2	2637	10	US-09-815-242-9859	Sequence 9859, Ap
35	136	3.2	8493	9	US-10-071-766-51	Sequence 51, Appl
36	135.5	3.2	2526	9	US-09-938-824A-1242	Sequence 1242, Ap
37	132	3.1	10300	10	US-09-960-253-145	Sequence 145, App
38	130.5	3.1	6750	9	US-09-866-557A-3	Sequence 3, Appl
39	130	3.0	6604	10	US-09-891-368-55	Sequence 55, Appl
40	126.5	3.0	7497	10	US-09-960-253-175	Sequence 175, App
41	125.5	2.9	2792	12	US-10-044-070-579	Sequence 579, App
42	125	2.9	2968	10	US-09-815-242-4796	Sequence 4796, Ap
43	125	2.9	3030	10	US-09-815-242-8043	Sequence 8043, Ap
44	124.5	2.9	3237	9	US-10-071-766-39	Sequence 39, Appl
45	123.5	2.9	1967	10	US-09-864-761-4793	Sequence 4793, Ap

ALIGNMENTS

RESULT 1
US-09-469-522-34
: Sequence 34, Application US/09469522
: Patent No. US20020151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Burke
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM pc compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.40
: CURRENT APPLICATION NUMBER: US/09/469,522
: FILING DATE: 22-Dec-1999
: CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Bidler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTXC:506
 TELEPHONE/COMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3266 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURES:
 NAME/KEY: CDS
 LOCATION: 7..2502
 SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 US 09 459-522-34

Alignment Scores:

Prod. No.: 0 Length: 3266
 Score: 4278.00 Matches: 832
 Percent Similarity: 100.00% Conserved: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09 026-459a-35 (1-832) x US 09 459 522-34 (1-3266)

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 QY 41 GluIleAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAsp 60
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 DB 247 CGGAGATTTGATATCTACTCAATATAATTTGTATTGTTGTTGTTGTTGTTGTTGTTG 306
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RESULT 3

US-09-459 522-30

Sequence 30, Application US/09469522

Patent No. US20050151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Hendrick, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Burkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Paton to release #1.0, Version #1.40
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/469,522
 FILING DATE: 22 Dec 1999
 CLASSIFICATION: (Unknown)
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: (Unknown)
 AIRNEY/AGENT INFORMATION:
 NAME: Bibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: 01X:506
 TELEPHONE: 512/418-4000
 TELEFAX: 512/474-7777
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHAPACTERISTICS:
 LENGTH: 4392 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 FEATURE:
 NAME/KEY: CUS
 LOCATION: 7...2628
 SEQUENCE DESCRIPTION: SEQ ID NO: 40:
 US 09-469,522 40

Alignment Scores:
 Seq. No.: 0 Length: 4392
 Score: 4274.00 Matches: 831
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.88% Indels: 0
 LB: 10 Gaps: 0

US 09-026-459A 35 (1-832) x US-09-459-522-30 (1-4392)

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DB 1690 GTGAATGGGTTTAAATTAAAGGCTTTTATTTTAAAGTATGATGAAAGTTTATACAAA 1749
QY 442 AlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 461
DB 1760 GCAAAAGGAAACATGACAAACAGAAATCAATAAAACATTTAGAACGATGCAACATCGAATC 1809
QY 462 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLys 481
DB 1810 ATGAATGGCTTGCATGAGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAAATCAAG 1869
QY 482 AspArgGlnIlePheProThrAspHisMetSerAlaGlySerIleLeuAsnLeuProLeuGlu 501
DB 1870 GAAGAAAGAAAGAAATATATATATATATATATATATATATATATATATATATATATAT 1929
QY 502 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysGly 521
DB 1940 AATAAATCAATCTGACACATATATATATATATATATATATATATATATATATATATATAT 1989
QY 522 SerThrThrArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAlaPheGln 541
DB 1990 TCAATATAGCTGTAAATTTATATATATATATATATATATATATATATATATATATATATAT 2049
QY 542 ThrGlnLysProLysSerThrSerLeuSerLeuPheTyrLysLysValIleArgLeu 561
DB 2060 ACCAAGAGCATTAATATATATATATATATATATATATATATATATATATATATATATAT 2109
QY 562 AlaTyrLeuArgLeuAsnThrLeuGlyGlyArgLeuLeuSerGluHisProLysLeuGlu 581
DB 2110 GGCATATATCCGGTAAATATATATATATATATATATATATATATATATATATATATATAT 2169
QY 582 HisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluIleLeuMetArgAsp 601
DB 2170 CATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2229
QY 602 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyThrCysLysValIleAsnGly 621
DB 2240 AAGATTTGAAATATATATATATATATATATATATATATATATATATATATATATATATAT 2289
QY 622 AsnLeuLysPheLysIleIleValThrAlaTyrLysAsnLeuProHisAlaValIleGln 641
DB 2290 GAGCTTAAATTCAGAAATCATATTAACATATATATATATATATATATATATATATATATATAT 2349
QY 642 ThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 661
DB 2450 AATTCAGAAAGTATATATATATATATATATATATATATATATATATATATATATATATAT 2499
QY 662 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgPro 681
DB 2410 TGGTCTCTATGAGAGATATATATATATATATATATATATATATATATATATATATATATAT 2469
QY 682 ThrLeuSerProIleProHisIleProAcqSerProTyrIlePheProSerSerProLeu 701
DB 2470 ACCCTTGACCAATACCTTCACATTCCTCGAAGCCCTTACAGTTTCTTAGTTCACCCCTTA 2529
QY 702 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGlu 721
DB 2500 GGAATTCATGAGAGAAATATATATATATATATATATATATATATATATATATATATATATAT 2589
QY 722 GlyLeuProThrProIleLysMetThrProArgSerArgIleLeuValSerIleGlyGlu 741
DB 2590 GGTTCGCAACACAAACAAATATGATCCCAAGATCAAGAAATCTTAGTATCAATTGGTAA 2649

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QY 742 SerPheGlyThrSerGluLysPheGlyIleAsnGlnMetValIleAsnSerArgAsp 761
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QY 782 AspIleGluLysSerAspGluAlaAspGlySerLysHisLeuProLeuGluSerLysPhe 801
DB 2770 CATATGCAAGATCATATGAACTAGAGAAATCAACAATCCCAACACACATCCCAAAA 2829
QY 802 GlnGlnLysLeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnMetAsn 821
DB 2840 CACCAAAATATGACAAATATATATATATATATATATATATATATATATATATATATATAT 2889
QY 822 AspSerMetAspThrSerAsnLysGlnGluLys 842
DB 2890 CATATGCAAGATCATATGAACTAGAGAAATCAACAATCCCAACACACATCCCAAAA 2949

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RESULT 8

US-09-469-522-50

Sequence 50, Application US/09469522

Patent No. US29020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Renedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.33

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: 22-Dec-1999

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hiblot, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 3554 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 7..2790

SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-09-469-522-50

Alignment Scores:

Pred. No.:

0

4263.00

Length:

3554

Matches:

829

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/474-3000
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:
LENGTH: 3461 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURES:

NAME/KEY: CDS
LOCATION: 7...2697

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US 09 469 522-40

ALIGNMENT SCORES:

Seq. No.: 0 Length: 3461
Score: 4217.00 Matches: 821
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Gap: 0 Gaps: 0

US 09 026 459a-35 (1-832) x US-09-469-522-40 (1-3461)

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33 GTCGACATAGACAGATGCGTACATTTACTGAGCTACACAAACATACAAATCAGT
34 ValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAla
35 GTCGACATAGACAGATGCGTACATTTACTGAGCTACACAAACATACAAATCAGT
36 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuIleArg
37 ATGCAACACGTTGAGGAGATATATGATTTTGTGACTTCTTCTGACTTCTGACTTCT
38 ThrCysGluLeuLeuTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSer
39 ACAATGCAACATATAATTTGACACAAACACAGCTGATATCTACATCTACATCTAC
40 AlaLeuValLeuLeuValSerTrpPheLeuLeuAlaLysGluValLeuGln
41 GATGAGGCTAAGAAATTTCTTGATATATTTTATTTATTTATTTATTTATTTATTTAT
42 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle
43 ATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
44 LysLeuSerProMetLeuLeuLysGluPheTyrLysThrAlaValIleProIleAsn
45 AAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
46 GlySerProArgThrProArgArqGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu
47 GATTCACCTGAC
48 GluAspThrArqIleIleGluValIleCysLysGluHisGluCysAsnIleAspGlu
49 GAATATGATACAGATATATGATATATGATATATGATATATGATATATGATATATGAT
50 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGluValThr
51 GTCGACATAGACAGATGCGTACATTTACTGAGCTACACAAACATACAAATCAGT
52 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys
53 TCTAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
54 AsnLysAspLeuAspAlaArqLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer
55 AATAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
56 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleValThrAla

252 IleAspSerPheGluThrGluArgThrPheAlaLysSerAsnLeuAspGluValAsn
253 ATACACAGCTTTGAAACACAGACACACACACACACACACACACACACACACACACAC
254 ValIleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMet
255 GTAAATTCCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT
256 IleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys
257 ATAAAAACAGCAAGTATCAACGATCAACGATCAACGATCAACGATCAACGATCAACGAT
258 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys
259 ACAGTCAATCCCAACAACTATACGAAACAGATGAGGATATAGCAATCAATCAATCAAT
260 GluLysPheAlaLysAlaValGlyGlnCysValGlnIleGlySerGluArgTyrLys
261 GAGAAATTTCTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
262 LeuGlyValArgIleSerTyrArgValMetGluSerMetLeuLysSerGluGluArg
263 CTTCGAGTTCGCTTGTATTTACCGATATGGAATCCATTCCTTAAATCAGACAGAAACA
264 LeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheIleMetSerLeuLeu
265 TTATCCATCAAAATTTAGCAAACTCTGATGATGATGATGATGATGATGATGATGATGAT
266 AlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGluAsnLeuAsp
267 GGTGCGGCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
268 SerGlyThrAspLeuSerPheTrpPheLeuAsnValLeuAsnLeuLysAlaPheAsp
269 TCGGACACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
270 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle
271 TTATCAAAATTCGATCAAAAGTTTATCAAAACAGACAGACACACACACACACACACAC
272 LysHisLeuLeuArgCysSerHisArgIleMetGluSerLeuAlaTrpLeuSerAspSer
273 AAACATTTAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
274 ProLeuPheAspLeuIleLysGlnSerTyrAspArgGlyGlyProThrAspHisLeuGlu
275 CATTATTTCACTTATTAACAAATCAAAACACACACACACACACACACACACACACACAC
276 SerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu
277 TCGCTTGTGCTCTTAACTTCT
278 SerProValArgSerProLysTyrLysGlySerThrArgValAsnSerThrAlaAsn
279 TCTCTCTGTAGATCTCCCAAGAAAAAGGTTCACTAGCGGTGTAATTTCTACTGCAAAAT
280 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu
281 GAGACACACAAAC
282 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuGluGlu
283 TCACTTTTATAAAAAGTGTATCGGCTATCGCTATCTCCGCTAAAATACACTTTGTCAA
284 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGluHisThr
285 GGTTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
286 LeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer
287 CTGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
288 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleValThrAla

QY 217 GluValGluAsnLeuSerLysArgTyrGluGluTleTyrLeuLysAspLeuAsp 236
DB 218 CACCCAGATTAGAAATATATCATCTGGACCCCTTCCAGACACCCCTGAGAAATGATAT 1746
QY 597 GluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyLys 616
DB 1747 CAATTCATGACAGACACACCATTTGGACCAAAATATGATGCTGCTCCAGATGCAAGCA 1806
QY 517 LysValLysAsnIleAspLeuLysPheLysLysLysLysLysLysLysLysLys 646
DB 1807 AAAGTCAGAAATATAGACCTTAAATTTCAAAATCATTTGTAATAGCAATAGCAATGCTTCT 1856
QY 637 HisAlaValGluGlnThrPheLysArgValLeuLysLysLysLysLysLysLys 656
DB 1867 CATGCTGCTTCAAGCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1926
QY 657 IleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAla 676
DB 1927 ATAGTATTTCTATTAATTCGGCTGCTGACAGACATCAAAACAAATATTTTCAGATGCT 1986
QY 677 SerThrArgProProThrLeuSerProIleProHisIleProArgSerProTyrLysPhe 696
DB 1987 TCACACCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2046
QY 697 ProSerSerProLeuArgIlePheGlyGlyAsnIleTyrIleSerProLeuLysSerPro 716
DB 2047 GCTAGTTCATGCTTCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2106
QY 717 TyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIleLeu 736
DB 2107 TATTAATTTTCAAGAGCTGCTCAACACCAACCAAAATACATCCCAAGATCAAGAAATGTA 2166
QY 737 ValSerIleGlyLysSerPheGlyThrSerGluLysPheGluLysIleAsnGlnMetVal 756
DB 2167 GATCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTG 2226
QY 757 CysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProProLysProLeu 776
DB 2227 TGTTCAGAGCAAGCTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAAT 2286
QY 777 LysLysLeuArgPheAspIleGlySerAspGluLysAspGlySerLysLeuPro 796
DB 2287 AAAAAATACCTTTTTCATATTCAGAGCAAGCTTCTGCAATTTCTGCAATTTCTGCAATTT 2346
QY 797 GlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlu 816
DB 2347 GAGAGTCTCAAAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAAT 2406
QY 817 LysGlnLysMetAspAspSerMetAspThrSerAsnLysGluGlyLys 842
DB 2407 AAGTCAAAATTAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2454

RESULT 12
US-09-469-522-36
Sequence 36 Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: XU, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: METASTATIC FETINOBLASTOMA TUMOR SUPPRESSOR
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

QY 217 GluValGluAsnLeuSerLysArgTyrGluGluTleTyrLeuLysAspLeuAsp 236
DB 218 CACCCAGATTAGAAATATATCATCTGGACCCCTTCCAGACACCCCTGAGAAATGATAT 1746
QY 597 GluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyLys 616
DB 1747 CAATTCATGACAGACACACCATTTGGACCAAAATATGATGCTGCTCCAGATGCAAGCA 1806
QY 517 LysValLysAsnIleAspLeuLysPheLysLysLysLysLysLysLysLysLys 646
DB 1807 AAAGTCAGAAATATAGACCTTAAATTTCAAAATCATTTGTAATAGCAATAGCAATGCTTCT 1856
QY 637 HisAlaValGluGlnThrPheLysArgValLeuLysLysLysLysLysLysLys 656
DB 1867 CATGCTGCTTCAAGCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1926
QY 657 IleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAla 676
DB 1927 ATAGTATTTCTATTAATTCGGCTGCTGACAGACATCAAAACAAATATTTTCAGATGCT 1986
QY 677 SerThrArgProProThrLeuSerProIleProHisIleProArgSerProTyrLysPhe 696
DB 1987 TCACACCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2046
QY 697 ProSerSerProLeuArgIlePheGlyGlyAsnIleTyrIleSerProLeuLysSerPro 716
DB 2047 GCTAGTTCATGCTTCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2106
QY 717 TyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIleLeu 736
DB 2107 TATTAATTTTCAAGAGCTGCTCAACACCAACCAAAATACATCCCAAGATCAAGAAATGTA 2166
QY 737 ValSerIleGlyLysSerPheGlyThrSerGluLysPheGluLysIleAsnGlnMetVal 756
DB 2167 GATCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTG 2226
QY 757 CysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProProLysProLeu 776
DB 2227 TGTTCAGAGCAAGCTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAAT 2286
QY 777 LysLysLeuArgPheAspIleGlySerAspGluLysAspGlySerLysLeuPro 796
DB 2287 AAAAAATACCTTTTTCATATTCAGAGCAAGCTTCTGCAATTTCTGCAATTTCTGCAATTT 2346
QY 797 GlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlu 816
DB 2347 GAGAGTCTCAAAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAAT 2406
QY 817 LysGlnLysMetAspAspSerMetAspThrSerAsnLysGluGlyLys 842
DB 2407 AAGTCAAAATTAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2454


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612 LeuGlnAsnGlnGluGluMetArgAspArgHisLeuAspGlnIleMetMetCysSer 611
1627 CTGAGAAATAGATATATATATACAGACAGACAGATTTGACCAATATATATATGTTTC 1686
612 MetTyrArgHisGlnGlnValLysAsnIleAspLeuLysPheLysIleLeuValThrAla 631
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632 TyrLysAspLeuPheHisAlaValGlnGlnThrPheLysArgValIleLeuLysGluGlu 651
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652 GluThrAspSerIleLeuValPheLysValSerValPheMetGluThrGluLysThrAsn 671
1807 GAGTATGATCTATATATATATATATATATATATATATATATATATATATATATAT 1866
672 IleGluGlnIleAlaSerThrArgProThrProThrLeuSerProIlePheHisIleProArg 691
1867 AATTTGAGTATGATCTATATATATATATATATATATATATATATATATATATATAT 1926
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712 ProLeuLysSerProTyrTyrLysIleSerGluGluGluProThrProThrLysMetThrPro 731
1987 GCGCTAAGAGTGCATATATATATATATATATATATATATATATATATATATATATAT 2046
742 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 751
2047 AGATCAACAAATATATATATATATATATATATATATATATATATATATATATATATAT 2106
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2107 AIAAAACAGATGCTATACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 2166
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2167 GCTGCTAAGACAGTGAAGAAATATGCTTTGATATATATATATATATATATATATATAT 2226
792 SerLysHisIleuProGlyGluSerLysPheGlnGlnLysLysLysLysLysLysLysLys 811
2227 AGTAAACATCTCCACACACACACACACACACACACACACACACACACACACACACACAC 2286
812 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 831
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832 Lys 832
247 AAA 2449

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US-09-026-459a-35 (1-832) x US-09-459-522-46 (1-3377)

Sequence 46, Application US/09469522

Patent No. US2002015461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkne

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-459-522
 FILING DATE: 22-Dec-1999
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: Unknown
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REFERENCE/DOCKET NUMBER: 41,071
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3377 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2613
 SEQUENCE DESCRIPTION: SEQ ID NO: 46:
 US-09-459-522-46

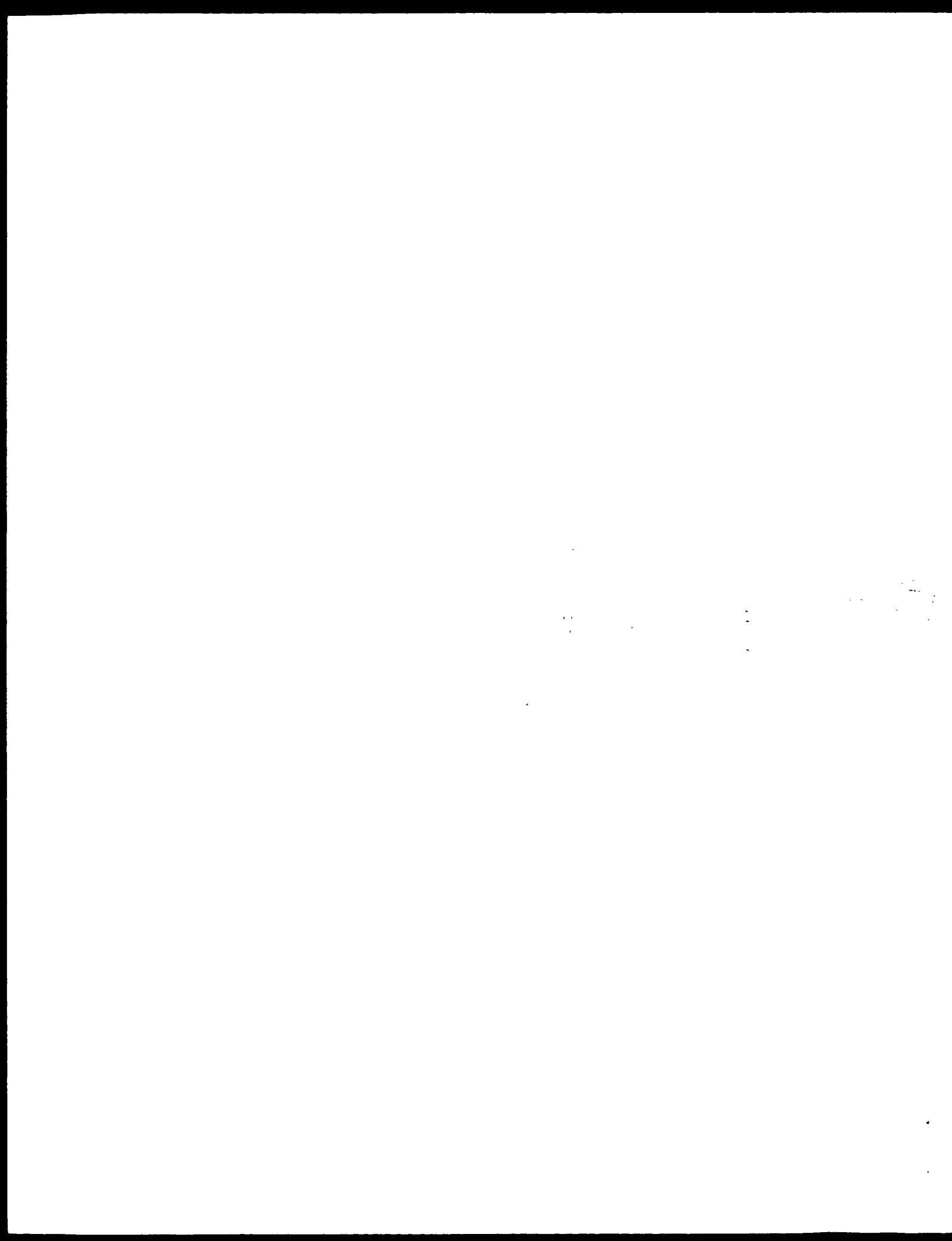
Alignment Scores:
 Pred. No.: 0 Length: 3377
 Score: 3930.50 Matches: 770
 Percent Similarity: 92.78% Gaps: 1
 Best Local Similarity: 92.68% Mismatches: 1
 Query Match: 91.88% Indels: 59
 DB: 10 Gaps: 1

US-09-026-459a-35 (1-832) x US-09-459-522-46 (1-3377)

QY 2 LeuTrpGlyIleCysIlePheIleAlaValAspLeuAspGluMetSerPheThrPhe 21
 DB 298 CTCTGCTGAAATCTGATTTTATGAGAGAGTTGACCTAGAGATGCGTTCACITTT 357
 QY 22 ThrGluLeuGlnLysAsnIleGluIleSerValIleLysIlePheAsnLeuLeuLysGlu 41
 DB 358 ACTGAGCTATAGAAAAACATAGAAATCAGTGCCATATAATTCCTTAAGCTTAATAAGAA 417
 QY 42 IleAspThrSerThrLysValAspAsnAlaMetSerArgIleuLysLysLysLysVal 61
 DB 418 ATTGATACCAAGTACCAAGTTGATATATGATGATATGATGATGATGATGATGATGAT 477
 QY 62 LeuPheAlaLeuPheSerLysLeuGluArgThrGlnLysGluLeuIleLysIleThrGlnPro 81
 DB 478 TTCTTTGCACTCTTCAGCAAAATGGAAGAGACACACGAACTTATATATTCACACAAACC 537
 QY 82 SerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
 DB 538 AGCAGTTCGATG----- 549
 QY 102 PheLeuLeuAlaLysGlyGluValIleuGlnMetGluAspAspLeuValIleSerPheGln 121
 DB 549 ----- 549
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 DB 549 ----- 549
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Search completed: January 19, 2003, 05:47:45
Job time : 140.745 secs



Genome version 5.1.1
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CM nucleic acid search, using sw model

Run on: January 14, 2003, 15:20:22 : Search time 92.4296 seconds
(without alignments)
16420.731 Million cell updates/sec

Title: US-09-026-459A 48
Perfected score: 4884
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Scoring table: IDENTITY_NUP
Gapop 10.0, Capexp 1.0

Searched: 93868 seqs, 22294149 residues
Total number of hits satisfying chosen parameters: 787745

Minimum DB seq length: 0
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Post processing: Minimum Match 100%
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Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4195.6	94.5	3555	10	US-09-469-522-1 Sequence 143, Appl
3	4194.6	94.4	4849	9	US-09-954-541-143 Sequence 50, Appl
4	4192.4	94.4	4554	10	US-09-469-522-50 Sequence 46, Appl
5	4169	93.7	3477	10	US-09-469-522-46 Sequence 28, Appl
6	4088.6	91.3	4455	10	US-09-469-522-28 Sequence 40, Appl
7	4024.6	89.4	4392	10	US-09-469-522-30 Sequence 32, Appl
8	2906.4	89.6	4461	10	US-09-469-522-40 Sequence 42, Appl
9	2956.6	87.4	4324	10	US-09-469-522-42 Sequence 34, Appl
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11	2898.6	85.7	3265	10	US-09-469-522-34 Sequence 3, Appl
12	2877.6	84.8	3424	10	US-09-469-522-38 Sequence 44, Appl
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ALIGNMENTS

RESULT 1
seq: 469 522 48
Sequence 48, Appl: 469 522 48

Patent No. US20020151461A1
GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433
CITY: Houston

STATE: TX
COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.40

CURRENT APPLICATION DATA: US-09-469-522

APPLICATION NUMBER: 22 Dec-1999

FILING DATE: 22 Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Hiblet, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTX:506

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-4000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 3483 base pairs
TYPE: nucleic acid

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GenCore version 5.1.3
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OM nucleic nucleic search, using SW model

Run on: January 16, 2003, 15:20:22 : Search time 60.7815 Seconds
(without alignments)
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Titles: US-09-026-459A-38

Perfect score: 4323
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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 49468 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4228	97.1	3461	10	US-09-459-522-40 Sequence 40, Appl
3	4224	97.1	3256	10	US-09-459-522-34 Sequence 34, Appl
4	4226	97.1	3323	10	US-09-459-522-42 Sequence 42, Appl
5	4226	97.1	3492	10	US-09-459-522-40 Sequence 40, Appl
6	4226	97.1	3455	10	US-09-459-522-28 Sequence 28, Appl
7	4226	97.1	3555	10	US-09-459-522-11 Sequence 11, Appl
8	4226	97.1	3459	9	US-09-954-531-143 Sequence 143, Appl
9	4222.8	97.0	3554	10	US-09-459-522-50 Sequence 50, Appl
10	4212	96.7	3218	10	US-09-459-522-31 Sequence 31, Appl
11	4107	93.5	3113	10	US-09-459-522-46 Sequence 46, Appl
12	4066.2	92.3	3347	10	US-09-459-522-42 Sequence 42, Appl
13	2867.6	86.3	3383	10	US-09-459-522-48 Sequence 48, Appl
14	2855.6	85.9	3377	10	US-09-459-522-46 Sequence 46, Appl
15	2837.4	85.1	3161	10	US-09-459-522-44 Sequence 44, Appl
16	2529.4	76.1	2995	10	US-09-860-211-7 Sequence 7, Appl
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18	142.2	4.3	411	10	US-09-864-761-4131 Sequence 4131, Ap
19	129	3.9	129	10	US-09-864-761-19910 Sequence 19910, A

ALIGNMENTS

RESULT 1

US-09-459-522-38

: Sequence 38, Application US/09469522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: Hu, Shi-Xue

: Benedict, William F.

: Zhou, Yu-Li

: TITLE OF INVENTION: Modified RETINOLASTOMA 10MER SUPPRESSOR

: PROTEINS

: NUMBER OF SEQUENCES: 51

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Arnold, White & Durkee

: STREET: P.O. Box 4433

: CITY: Houston

: STATE: TX

: COUNTRY: USA

: ZIP: 77210-4433

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent in Release #1.0, Version #1.40

: CURRENT APPLICATION DATA: US/09/469-522

: APPLICATION NUMBER: US/09/469-522

: FILING DATE: 22-Dec-1999

: CLASSIFICATION: <unknown>

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 09/026,459

: FILING DATE: <unknown>

: ATTORNEY/AGENT INFORMATION:

: NAME: Hilder, David W.

: REGISTRATION NUMBER: 41,071

: REFERENCE/WORK KEY NUMBER: UIN:506

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 512/418-3000

: TELEFAX: 512/474-7577

: INFORMATION FOR SEQ ID NO: 48:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 3323 base pairs

: TYPE: nucleic acid

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Sequence 2546, Ap
Sequence 1, Appl1
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Sequence 342, App
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Sequence 11218, A
Sequence 14521, A
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Sequence 154, App
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Sequence 4050, Ap
Sequence 749, App
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Genature version 5.1.4
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OM nucleic nucleic search, using sw model

Run on: January 16, 2003, 15:20:22, Search time 92.2567 Seconds
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16420.731 Million cell updates/sec

Title: us 09 026-459a-46

Perfect score: 4377

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- 3: /cenz_6/ptdata/a1/pubpna/us06_NEW_PUB.seq.*
- 4: /cenz_6/ptdata/a1/pubpna/us06_PUBOMB.seq.*
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- 10: /cenz_6/ptdata/a1/pubpna/us09_PUBOMB.seq.*
- 11: /cenz_6/ptdata/a1/pubpna/us10_NEW_PUB.seq.*
- 12: /cenz_6/ptdata/a1/pubpna/us10_PUBOMB.seq.*
- 13: /cenz_6/ptdata/a1/pubpna/us10_PUBOMB.seq.*
- 14: /cenz_6/ptdata/a1/pubpna/us06_PUBOMB.seq.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	4182.6	94.2	4889	9	US 09 454-531-143
4	4180.4	94.2	4554	10	US 09 469-522 46
5	4169	93.8	4383	10	US 09 469-522 46
6	4111	92.1	4347	10	US 09 469-522 46
7	4076.6	91.1	4456	10	US 09 469-522 46
8	4012.4	89.2	4392	10	US 09 469-522 46
9	2984.4	88.4	4411	10	US 09 469-522 46
10	2944.6	87.2	4323	10	US 09 469-522 46
11	2935	86.9	4361	10	US 09 469-522 46
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14	2841.6	84.1	4238	10	US 09 469-522 46
15	2825	83.7	4313	10	US 09 469-522 46
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17	428	12.7	451	9	US 09 796-692-7749
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19	129	3.8	129	10	US 09 864-761-19910

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25	49.4	1.5	640681	10	US 09 790 988 1
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ALIGNMENTS

RESULTS 1

Sequence 46, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED ROLINBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210 4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UIXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 542/418 3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 3477 base pairs

TYPE: nucleic acid

[illegible]


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RESULT 3

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: Sequence 143, Application US/09954531
: Patent No. US20020165180A1
: GENERAL INFORMATION:
: APPLICANT: Weaver, Zoe
: TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
: FILE REFERENCE: Gene Sets
: CURRENT APPLICATION NUMBER: US/09/954, 531
: CURRENT FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: US/60/234, 133
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: US/60/234, 009
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: US/60/234, 034
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: US/60/234, 509
: PRIOR FILING DATE: 2000-09-22
: PRIOR APPLICATION NUMBER: US/60/234, 567
: PRIOR FILING DATE: 2000-09-22
: NUMBER OF SEQ ID NOS: 1392
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 143
: LENGTH: 4839
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: ORGANISM: Homo sapiens
US-09-954-531-143
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Host Local Similarity 94.9% Prod. No. 0;
Matches 3372; Conservative 0; Mismatches 4; Indels 177; Gaps 1;
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[illegible]

REFERENCES

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Sequence 32, Application US/09469522

; Patent No. 152002015146, 1A1

E-MAIL: INFO@KMAI.LIN:

APPLICANT: XU, Hong Ji

$$H_0, S_H, X_{H_0}$$

Benedict, William F.

Z. Hong, Y. Huo and

$$I = \int_{\mathbb{R}^n} \left(\frac{1}{2} |\nabla u|^2 - \frac{1}{2} \lambda u^2 \right) dx$$
[illegible]

NUMBER OF SEQUENCES: 51

THE PRESIDENT'S ADDRESS:

ADDRESSEE: A
CITY: D

STEFAN: D. D.
STEFAN: H. H.

APPENDIX: HISTORY STATE: IX

STAFF: 1X
COUNTRY: USA

```

1  COMPUTER RELEASABLE FORM:
2
3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  SOFTWARE: Patent In Release #1.0, Version #1.1.40
7
8  CURRENT APPLICATION DATA:
9
10 APPLICATION NUMBER: US-09/469,522
11 FILING DATE: 22-Dec-1999
12 CLASSIFICATION: <Unknown>
13
14 PRIOR APPLICATION DATA:
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16 APPLICATION NUMBER: 09/026,459
17 FILING DATE: <Unknown>
18 ATTORNEY/AGENT INFORMATION:
19
20 NAME: Hibler, David W.
21 REGISTRATION NUMBER: 41,071
22 REFERENCE/DOCKET NUMBER: 01X:506
23
24 TELECOMMUNICATION INFORMATION:
25
26 TELEPHONE: 512/418-3000
27 TELEFAX: 512/474-7577
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29 INFORMATION FOR SEQ ID NO: 42:
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31 SEQUENCE CHARACTERISTICS:
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33 LENGTH: 323 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: Linear
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38 FEATURE:
39
40 NAME/KEY: CDS
41 LOCATION: 7..2559
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43 SEQUENCE DESCRIPTION: SEQ ID NO: 42:
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45 US-09-469,522-32

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Query Match

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Best Local Similarity	94.58	Pred. No.	0	

Matches 3134; Conservative 0; Mismatches

[illegible]

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148	3309	AGCAATATGATAGT	3423

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1  RESULT 11
2  US 09 469 522 44
3  Sequence 44, Application 05/0746,522
4  Patent No. US2002019461A1
5  GENERAL INFORMATION:
6  APPLICANT: Xu, Bona Ji
7  Ho, Shi Xue
8  Benedict, William F.
9  Zhou, Yongli
10 TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR
11 PROTEINS
12 NUMBER OF SEQUENCES: 51
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Arnold, White & Dorkes
15 STREET: P.O. Box 4433
16 CITY: Houston
17 STATE: TX
18 COUNTRY: USA
19 ZIP: 77210-4433
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: floppy disk
22 COMPUTER: IBM pc compat file
23 OPERATING SYSTEM: PC-DOS/MS-DOS
24 SOFTWARE: Patent In-Release #1.0, Version #1.40
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US2004/469,522
27 FILING DATE: 22-Dec-1999
28 CLASSIFICATION: unknown
29 PRIORITY APPLICATION DATA:
30 APPLICATION NUMBER: 09/026,459
31 FILING DATE: unknown
32 AGENCY/AGENT INFORMATION:

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Command line parameters:

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3	4401,5	98,8	4859	9 US 09-954-541-143 Sequence 143, App
4	408,5	98,8	3554	10 US 09 459-522-50 Sequence 50, Appl

5	4391,5	98,6	2095	10 US 09 860-211-7 Sequence 7, Appl
6	4240	95,2	3461	10 US 09-459-522-40 Sequence 40, Appl
7	4213,5	94,6	3455	10 US 09-459-522-28 Sequence 28, Appl
8	4142	93,0	3477	10 US 09 459-522-46 Sequence 46, Appl
9	4103,5	92,2	3392	10 US 09 459-522-40 Sequence 40, Appl
10	4103	92,1	3161	10 US 09 459-522-44 Sequence 44, Appl
11	4052	91,0	3183	10 US 09 459-522-48 Sequence 48, Appl
12	4037	90,0	3423	20 US 09 459-522-48 Sequence 48, Appl
13	3971,5	89,2	3423	10 US 09 459-522-42 Sequence 42, Appl
14	3877,5	87,1	3266	10 US 09 459-522-44 Sequence 44, Appl
15	3858,5	86,6	3218	10 US 09 459-522-43 Sequence 43, Appl
16	3850	86,5	3113	10 US 09 459-522-46 Sequence 46, Appl
17	766,5	17,2	3660	9 US 09-292-738-37 Sequence 37, Appl
18	516,5	11,6	3747	10 US 09 770-657-1 Sequence 1, Appl
19	516,5	11,6	3747	12 US 10 025-676-2 Sequence 2, Appl
20	355	8,0	3209	10 US 09 226-391-4 Sequence 4, Appl
21	243	5,5	411	10 US 09-864-761-131 Sequence 31, Appl
22	238	4,9	129	10 US 09-864-761-19910 Sequence 19910, A
23	177,5	4,0	404	10 US 09-964-824A-296 Sequence 296, App
24	151	3,4	6773	10 US 09-864-864-436 Sequence 436, App
25	145,5	3,3	424	9 US 09 795-692-2546 Sequence 2546, Ap
26	143,5	3,2	10096	10 US 09-960-253-163 Sequence 163, App
27	143,5	3,2	10190	10 US 09-864-864-292 Sequence 292, App
28	143,5	3,2	10211	10 US 09-954-456-1154 Sequence 1154, Ap
29	143,5	3,2	10211	10 US 09-967-768A-186 Sequence 186, App
30	141	3,2	4754	10 US 09 982-091A-1 Sequence 1, Appl
31	138,5	3,1	2637	10 US 09-815-242-9859 Sequence 9859, Ap
32	133	3,0	4457	10 US 09-960-253-154 Sequence 154, App
33	131	2,9	4302	10 US 09-801-368-59 Sequence 59, Appl
34	130,5	2,9	3624	9 US 10 108-605-216 Sequence 216, App
35	130	2,9	2525	9 US 09 938-842A-1242 Sequence 1242, Ap
36	130	2,9	5864	10 US 09-864-864-305 Sequence 305, App
37	130	2,9	8948	10 US 09-735-705-119 Sequence 119, App
38	130	2,9	8948	10 US 09-850-716A-119 Sequence 119, App
39	130	2,9	8948	10 US 09 847-738-119 Sequence 119, App
40	130	2,9	9588	10 US 09-954-456-1848 Sequence 1848, Ap
41	129,5	2,9	8493	9 US 10 071-766-31 Sequence 51, Appl
42	128,5	2,9	6886	9 US 10-098-841-40 Sequence 40, Appl
43	128	2,9	7893	9 US 10-077-130-3 Sequence 3, Appl
44	128	2,9	8106	9 US 10 077-130-1 Sequence 1, Appl
45	128	2,9	23907	9 US 10 077-140-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US 09-459-522-42
Sequence 42, Appl 11:31:15, P. 2, 34*52...
Patent No. US 2001/0151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong Ji
Ho, Shi Xue
Benedict, William F.
Zhou, Yuli

TITLE: INVENTION OF A METHOD FOR DETECTING BLAST-MA FORMER SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCE: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Apt 11, White's Drive
CITY: Houston
STATE: TX

COUNTRY: USA

ZIP: 77210-4434

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Release #1.0, Version #1.40

APPLICATION NUMBER: 02/07/459, 522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <Unknown>

SEQUENCE CHARACTERISTICS:
 LENGTH: 3455 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 topology: linear

FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2691
 SEQUENCE DESCRIPTION: SF010 NO: 28;
 US 09 026-459a-43

Alignment Scores:
 Pred. No.: 0 Length: 3455
 Scores: 4213.50 Matches: 824
 Percent Similarity: 92.17% Conserved: 0
 Best Local Similarity: 92.17% Mismatches: 1
 Query Match: 94.62% Indels: 64
 Gaps: 1

US 09 026-459a-43 (1-859) x US 09 469 522 28 (1-3455)

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1690  CCGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1749
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1810  GCGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1869
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US 09 469 522 40
 ? Sequence 30, Application US/09469522
 ? Patent No. US20020151461A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Xu, Hong Ji
 ? Hu, Shi Xue
 ? Schroeder, William F.
 ? Zhou, Yunli
 ? TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR
 ? PROTEINS

NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210 4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.00

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/459,522
 FILING DATE: 22 Dec 1999
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Hubert, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTX:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/474 8000
 TELEFAX: 512/474 7577

INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4392 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURES:
 NAME/KEY: CDS
 LOCATION: 7..4328
 SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US 09 469 522 40

Alignment Scores:
 Prod. No.: 0 Length: 4392
 Score: 4104.50 Matches: 803
 Percent Similarity: 91.98% Conservative: 0
 Best Local Similarity: 91.98% Mismatches: 1
 Query Match: 92.15% Indels: 69
 Gaps: 10

US 09 026 459A 43 (1 859) x US 09 459 522 30 (1-3392)

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690 AATATAAGCTTAAATCAAAATCATTTTAAAGATATATATATATATATATATAT 2049
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QY 807 ArgPheAspIleGluGlySerAspGlnAlaAspGlySerLysHisIleProGlyGlnSer 826
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RESULT 10
US-09-469-522-44
: Sequence 44, Application US/09469522
: Patent No. US20020151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED PETIN/BLASTOMA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US-09-469,522
: FILING DATE: 22-Dec-1999
: CLASSIFICATION: <Unknown>
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 09/026,459
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: UICX:506
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO: 44:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3161 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..2397
: SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-469-522-44
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Pred. No.: 0 Length: 3161
Score: 4103.00 Matches: 797
Percent Similarity: 92.99% Conservative: 0
Best Local Similarity: 92.78% Mismatches: 0
Query Match: 92.14% Indels: 62
DB: 10 Gaps: 1

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FEATURE:
NAME/KEY: CDS
LOCATION: 7..2619
SEQUENCE DESCRIPTION: SEQ ID NO: 48
US-09-469-522-48
Alignment Scores:
Pred. No.: 0 Length: 3383
Score: 4052.00 Matches: 801
Percent Similarity: 86.31% Conservative: 0
Best Local Similarity: 86.31% Mismatches: 1
Query Match: 90.99% Indels: 126
DB: 10 Gaps: 3
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QY 112 112
DB 367 CTGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 426
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RESULT 11

US-09-469-522-48

Sequence 48: Application US/09/469522

Patent No. US2002015461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

Zhao, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-469-522

FILING DATE: 22-Dec-1999

CLASSIFICATION: C12N2501/00

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 3383 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

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106 2476 GCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2535
832 LeuAlaGluMetThrSerThrArgThrArgMetGluLysGluLysMetAsnAspSerMet 851
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852 AspThrSerAsnLysGluGlyLys 859
106 2596 GATACCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2619

```

RESULT 12

US-09-459-522-38

Sequence 38, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Hendrick, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433

QY 112 ----- 112
 DB 190 GATACAGTACCAAACTTCATTAAGCTTATGTCACAGACTTCGTCACAAAGTATGATGATTC 249
 QY 112 ----- 112
 DB 250 TTGGACATCTTCAGCAAAATTCAGAGAGACATCTGAATTTATATATATTTTCATCAACCTCAGC 309
 QY 114 ----- 114
 DB 330 SerThrGluIleAsnSerAlaIleValIleuLysValSerTrpIleThrPhe 129
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 QY 140 LeuLeuAlaIleLysGluValIleGlnMetGluAspSerLeuValIleSerPheGlnLeu 149
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 QY 170 TyrLysIleAlaValIleThrIleAsnGlySerProArgThrProArgAlaGlyGlnAsn 189
 DB 490 TATAAATACGTTATATATTAATAGTTCAATTAAGATTCAGATTAAGATTCAGATTCAGATTC 549
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 DB 550 AAGAGTACAGCAACCAAAATACACAAATGATACAAATTAATGAATTCCTCTGT 609
 QY 210 LysGluIleGlyCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePro 229
 DB 610 AATACATGATGATGATTAATATATATGATGATGATGATGATGATGATGATGATGATGATGAT 669
 QY 240 PheMetAsnSerLeuGlyLysValThrSerAsnGlyLeuProGluValGluAsnLeuSer 249
 DB 670 TTTATCAATCTCTTGACTGTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 729
 QY 250 LysArgTyrGlyGluIleTyrLeuLysAsnLysAspLeuAlaArgLeuPheLeuAsp 269
 DB 740 AAACGATACGAAGAAATTAATCTAAAAATAAAGATCTAGATGCAAGATTAATTTTGGAT 789
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QY 430 SerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIleLeu 449
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QY 469 AlaGluLysValLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 488
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QY 729 ArgIleProGlyLysAsnIleTyrHisSerThrLeuLysSerProTyrLysIleSerGlu 748
DB 2110 GATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 2169

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RESULT 15

US-09-469-522-3

Sequence 3, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/09469522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UIXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 3218 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 7..2454

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-469-522-3

GenScore version 5.1.3
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us-09-026-459a-44

us-09-026-459a-44
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Gapop 10.0, Gapext 1.0

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Gapop 10.0, Gapext 1.0

us-09-026-459a-44
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Gapop 10.0, Gapext 1.0

us-09-026-459a-44
Sequence: 1 GCGGTCATGCGGCGGAAAC.....AAATGAGGATTATTCATGAT 3161
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Gapop 10.0, Gapext 1.0

us-09-026-459a-44
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Gapop 10.0, Gapext 1.0

us-09-026-459a-44
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Gapop 10.0, Gapext 1.0

us-09-026-459a-44
Sequence: 1 GCGGTCATGCGGCGGAAAC.....AAATGAGGATTATTCATGAT 3161
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Gapop 10.0, Gapext 1.0

us-09-026-459a-44
Sequence: 1 GCGGTCATGCGGCGGAAAC.....AAATGAGGATTATTCATGAT 3161
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us-09-026-459a-44
Sequence: 1 GCGGTCATGCGGCGGAAAC.....AAATGAGGATTATTCATGAT 3161
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us-09-026-459a-44
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us-09-026-459a-44
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us-09-026-459a-44
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Scoring tables: IDENTITY NUC
Gapop 10.0, Gapext 1.0

ALIGNMENTS

RESULT 1

us-09-026-459a-44
Sequence 44, Application US/09469522
Patient No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Inu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED PPTIN-ELASTIN-MA COM-P SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCE: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Burke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.0

CURRENT APPLICATION DATA: US/09469522

APPLICATION NUMBER: US/09469522

FILING DATE: 22 Dec 1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

AUTHOR/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTX:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-6000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 3161 base pairs

TYPE: nucleic acid

us-09-026-459a-44
Sequence: 1 GCGGTCATGCGGCGGAAAC.....AAATGAGGATTATTCATGAT 3161
Scoring tables: IDENTITY NUC
Gapop 10.0, Gapext 1.0

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us-09-026-459a-44
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Gapop 10.0, Gapext 1.0

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100 3121 AAGAGTCTATATATATATTCAGAGGCTCTGGCAACAAACAAAATATGTCAGAGTCA 3180
100 3122 AAGAGTCTATATATATATTCAGAGGCTCTGGCAACAAACAAAATATGTCAGAGTCA 3180

QY 3121 CTTCATCCAACTTATCTTTTAAATGAGGATTATGATCT 3161
Db 3121 CTTCATCCAACTTATCTTTTAAATGAGGATTATGATCT 3161

RESULT 2

US-09-469-522-42
Sequence 42: Application: US/0469522
Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi Xue
Benedict, William F.
Zhou, Yuoli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA

ZIP: 77210 4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09469,522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 3347 base pairs

TYPE: nucleic acid

SWAPPEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 7..2584

SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-09-469-522-42

Query Match 93.8%; Score 2965; DB 10; Length 347;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 3161; Conservative 0; Mismatches 0; Indels 186; Gaps 1;

QY 1 CGGTCATGCGCGCAAAACCCCGCAAAATCGCGGCAACGCGGCGCGCGCGCGCGCG 60
Db 1 CGGTCATGCGCGCAAAACCCCGCAAAATCGCGGCAACGCGGCGCGCGCGCGCGCG 60
QY 61 GAACCG 120
Db 61 GAACCG 120
QY 121 CGGAG 180
Db 121 CGGAG 180
QY 181 GCATTATGTCAGAGAAATTAAGATACCGAGATCACTGTCAGAGAGAGAGAGAGAG 240

DB 2949 GGGGCGAAGTACGTCGCAAGGCAATTTTGAATGAGAGGCAATCAACAAAAATTAACG 3058
QY 2947 AATCTTTCTCAAAATGAT 2956
DB 3059 AATCTTTCTCAAAATGAT 3118
QY 2957 TACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3016
DB 3119 TACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3178
QY 3017 TTTTAAATTAATTAAGTATATATATATATATATATATATATATATATATATATAT 3076
DB 3179 TTTTAAATTAATTAAGTAT 3238
QY 3077 CAATTTTAT 3136
DB 3239 CAATTTTAT 3298
QY 3137 TTTTAAATTAATTAAGTATATATATATATATATATATATATATATATATATATAT 3196
DB 3299 TTTTAAATTAATTAAGTATATATATATATATATATATATATATATATATATATAT 3358

RESULT 8

US-09-469-522-38

Sequence 38, Application US/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

HU, Shi-Xue

Benedict, William P

Zhou, Yunli

TITLE OF INVENTION: M-GLIFED, PETIN-GLAST-MA 10M & SUPPRESSOR

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1 0, Version #1 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469, 522

FILING DATE: 22-Nov-1999

CLASSIFICATION: C06K 21/00

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: UNKNOWN

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTXC-506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 3323 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CUS

LOCATION: 7,12559

SEQUENCE DESCRIPTION: SEQ ID NO: 38.

US-09-469-522-38

Query Match 89.4% Score 2827.4: DB 10: Length 2323;
Best Local Similarity 99.6%: Pref No 0;
Matches 284, Conservative 6, Mismatches 11, Indels 8, Gaps 0;

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DB 479 TCAAGCAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 538
QY 377 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 436
DB 539 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 598
QY 437 AAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 496
DB 599 AAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 658
QY 497 ATTTAT 556
DB 659 ATTTAT 718
QY 557 AAGATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
DB 719 AAGATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 778
QY 617 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 676
DB 779 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 838
QY 677 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 736
DB 839 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 898
QY 737 TTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 796
DB 899 TTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 958
QY 797 AAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 856
DB 959 AAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1018
QY 857 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 916
DB 1019 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1078
QY 917 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 976
DB 1079 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1138
QY 977 GAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1036
DB 1139 GAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1198
QY 1037 AAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1096
DB 1199 AAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1258
QY 1097 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1156
DB 1259 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1318
QY 1157 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1216
DB 1319 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1378
QY 1217 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1276
DB 1379 TATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1438
QY 1277 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1336
DB 1439 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1498
QY 1437 AATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1496

Db 1457 CATGATTCGATGATGTTTAAATTAAGGCTTTGATTTTACAAAGTCATGAAAGTT 1516
QY 1217 TTAACAAATACAAAGCAATTTGAAACAGAGAAATGATAAAACATTTAAACGATGCAAC 1276
Db 1517 TATCAAAACAGAGGCACTTTCAGACAGAGAAATGATATAAAACATTTAGAGATGTGAAC 1576
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QY 1337 AATCAAAAG 1396
Db 1637 AATCAAAAG 1696
QY 1397 CTCTCTCAATAATATCAATATCAATATCAATATCAATATCAATATCAATATCAATATCA 1456
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QY 1697 TGAGAGATAGGCAATTTGAG 1756
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QY 1757 AGAATATAGAGCTTAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1816
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Db 2117 TTCAAG 2176
QY 1877 TCTAATAGCTGCTTCAAG 1936
Db 2177 TCTAATAGCTGCTTCAAG 2236
QY 1937 GAGGAGGCTTACCTTTCAG 1996
Db 2237 GAGGAGGCTTACCTTTCAG 2296
QY 1997 CAGGCTTACGAG 2056
Db 2297 CAGGCTTACGAG 2356
QY 2057 TTTCAAGAGGCTTTCAG 2116
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QY 2117 TTTGAG 2176
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QY 2357 AAATGAATGATAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2416
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QY 2417 GTGGACACGCTGTACAGCTCTGGATTCATGCTCTCACAGAGAGAGAGAGAGAGAGAG 2476
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Db 2777 CAGATCT 2836
QY 2537 CAGATCT 2596
Db 2837 CAGATCT 2896
QY 2597 CAAGATTCAGAAATCT 2656
Db 2897 CAAGATTCAGAAATCT 2956
QY 2657 TTTCAAAATGAAATTTCT 2716
Db 2957 TTTCAAAATGAAATTTCT 3016
QY 2717 GATACGAG 2776
Db 3017 GATACGAG 3076
QY 2777 CTGTCT 2836
Db 3077 CTGTCT 3136
QY 2837 CTGTCT 2896
Db 3137 CTGTCT 3196
QY 2897 ACT 2956
Db 3197 ACT 3256
QY 2957 TACATTTTATTTTCT 3016
Db 3257 TACATTTTATTTTCT 3316
QY 3017 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3076
Db 3317 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3376
QY 3077 CAGATTTTATCT 3136
Db 3377 CAGATTTTATCT 3436
QY 3137 TTTTAAATGAGGATTTATGATAGT 3161
Db 3437 TTTTAAATGAGGATTTATGATAGT 3461

RESULT 12

US-09-469-522-50

: Sequence 50, Application: US/09469522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

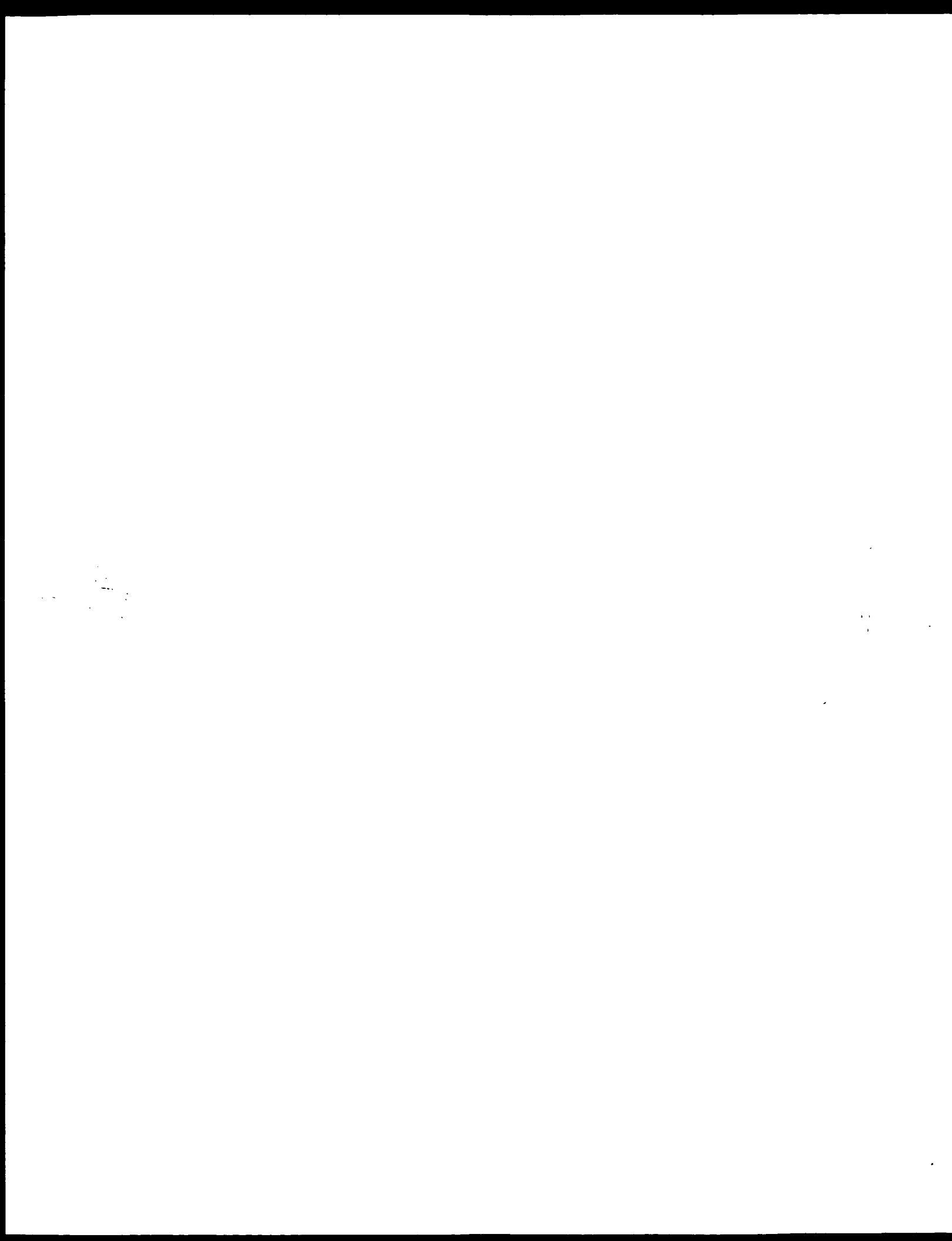
: APPLICANT: Xu, Hong-Ji

: Hu, Shi-Xue

: Benedict, William F.

: Zhou, Yunli

: TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR
: PROTEINS



PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: <UNKNOWN>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hiblet, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTXC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3161 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2397
 SEQUENCE DESCRIPTION: SEQ ID NO: 44

Alignment Scores:

Prod. No.: 6 Length: 3161
 Score: 4144.00 Matches: 797
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US 09-026-459A-45 (1-797) x US-09-469-522-44 (1-3161)

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 7 ATGCCGCCCAAAACCCGCGGAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 66
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 67 CCGGCG 126
 41 AspLeuProLeuValArgGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
 127 GAGCTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 186
 61 CysGlnLysLeuLysLeuProAspHisValArgGluGluGluGluGluGluGluGluGlu 80
 187 TGTGCAAAATTAAGATACCAATCATCTCAGACAGACAGACAGACAGACAGACAGACAG 246
 81 ValSerSerValAspGlyValLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 247 GHTTCACTGTGTGACGAGCTATGTGTGAGCTTATATTTAAAGAAAGAAAGAAAGAAAG 306
 101 ThrCysLeuPheLeuAlaAlaValAspLeuAlaValLeuProLeuAsnGlySerProArg 120
 307 ATCTGTATCTTTATTGCAAGATTAATGATGATGATGATGATGATGATGATGATGATGAT 456
 121 ThrProArgArgGlyGlnAsnArgSerAlaArgGlyGlyGlyGlyGlyGlyGlyGlyGly 140
 457 ACACCCAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
 141 ArgLeuLeuValLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160
 427 AGAATTTATTCAGATCT 486
 161 TyrPheLysAsnPheLeuProPheMetAsnSerLeuGlyGlyGlyGlyGlyGlyGlyGly 180
 487 TATTTCAAAATTTTATATCTTTTATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 546
 181 ProGluValGluAsnLeuSerLysArgGlyGluGluGluGluGluGluGluGluGluGlu 200
 547 CCAGAGGCTTCAAAATCTTCTTAAACCATACCAAGCAAAATTTATCTTTAAATAATTA 606
 201 AspAlaArgLeuPheLeuAspHisLysThrLeuGluThrAspSerIleAspSerPhe 220

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 221 GluThrGlnArgThrProArgLysSerAsnLeuAspGlyGlyGlyGlyGlyGlyGlyGly 240
 667 GAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAAT 726
 241 HisThrProValArgThrValMetAspThrIleGluGlnLeuMetMetIleLeuAspSer 260
 727 CACATCCAGTTAGACTGTTATGAACTATGCAACACTATGCAACAAATTAATCATCATTTAAATTC 786
 261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAspAspCysThrValAsnPro 280
 787 GAAATGATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCA 846
 281 LysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGlyLysPheAla 300
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 907 AAAGCTGTGCGACACAGCTGTGCGTGTGAAATTTGCAACAGGATACAAACTTGAGTTCGG 966
 321 LeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGln 340
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 341 AsnProSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
 1027 AATTTTACAAACTTCTGAATGACAACTTTTCAATATGATGATGATGATGATGATGATG 1086
 361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAsp 380
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 421 ArgCysGlnHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAsp 440
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 1327 CTATTTAAACAACAAAG 1386
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 1447 TCTCCAAAGAAAGAAAGTTCACATACCGTGTAAATTTCTACTGCAAAATGAGAGACAAA 1506
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 1507 GCAATCTAGCTTTCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCA 1566
 521 LysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSer 540
 1567 AAAAAAGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1626
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[illegible]

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> CLASSIFICATION: <Unknown>  

> PRIOR APPLICATION DATA:  

>   APPLICATION NUMBER: 09/626,459  

>   FILING DATE: <Unknown>  

> ATTORNEY/AGENT INFORMATION:  

>   NAME: Hibler, David W.  

>   REGISTRATION NUMBER: 41,971  

> REFERENCE/JACKET NUMBER: UIXC-506  

> TELECOMMUNICATION INFORMATION:  

>   TELEPHONE: 512/418-4000  

>   TELEFAX: 512/474-7577  

> INFORMATION FOR SEQ ID NO: 42:  

>   SEQUENCE CHARACTERISTICS:  

>     LENGTH: 3347 base pairs  

>     TYPE: nucleic acid  

>     STRANDEDNESS: single  

>     TOPOLOGY: linear  

> FEATURE:  

>   NAME/KEY: CDS  

>   LOCATION: 7..2583  

>   SEQUENCE DESCRIPTION: SEQ ID NO: 42:  

US-09-469-522-42
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Pred. No.:      0          Length:    3347  
Score:         4104.00       Matches:    797  
Percent Similarity: 92.78%    Conservative: 0  
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Query Match:    99.01%        Indels:     62  
DB:             10           Gaps:       1
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QY  101 HecYstIlcpheLIalaLaLavaspLeu----- 110  
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Db  367 CTCCTAAAAGTTCTTGGATCACATTTTTATTAANTLAAGGCGCAACTATTAATAATCCAA 426  
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QY 449 GluGlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeuProLeuGlnAsnAsn 468
DB 1567 GAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1525
QY 469 HisThrAlaAlaAspMetLysLeuSerProValArgSerProLysLysLysLysSerThr 488
DB 1627 CACACGACACACACACACACACACACACACACACACACACACACACACACACACACAC 1686
QY 489 ThrArgValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAlaPheGlnThrGln 508
DB 1687 ACCGGGCGTAAATTCATGCAAAATGACAGACACACAAAGCAAGCTCAGCCCTCCAGACCCAG 1746
QY 509 LysProLeuLysSerThrSerLysSerLysSerLysSerLysSerLysSerLysSerLys 528
DB 1747 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1806
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DB 1807 CTCCGCTTAAATACATCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1866
QY 549 IleTrpThrLeuPheGlnHisThrLeuGlnAsnGlnLysGlnLeuMetArgAspArgHis 568
DB 1867 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1926
QY 569 LeuAspThrLeuMetMetCysSerMetCysGlnLysGlnLysGlnLysGlnLysGln 588
DB 1927 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1986
QY 589 LysPheLysIleIleValThrAlaTrpLysAspLeuProHisAlaValGlnGlnThrPhe 608
DB 1987 AAATTCACATCATCTAACAGCAACACAGGATCTTCTGATGATGATGATGATGATGAT 2046
QY 609 LysArgValLeuLeuLysSerLeuGlnLysSerLeuLysSerLeuLysSerLeuLys 628
DB 2047 AAAGGCTGTTGATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2106
QY 629 PheMetGlnArgLeuLysThrAsnLeuGlnTrpLysThrArgProProThrLeu 648
DB 2107 TTGATGACAGAGATGAAATGAAATTTTGAATGATGATGATGATGATGATGATGAT 2166
QY 649 SerProIleProHisIleProAlaGlnSerProLysLysPheProLysSerProLeuArg 668
DB 2167 TCACTAAATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2226
QY 669 ProGlyLysAsnLeuLysLeuSerProLeuLysSerProLysLysSerProLysLys 688
DB 2227 CCGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2286
QY 689 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGlnSerPhe 708
DB 2287 GCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2346
QY 709 GlyThrSerGlnLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeu 728
DB 2347 GGGACCTGTCAGAGATGCCAGAAAATAATGATGATGATGATGATGATGATGATGATGAT 2406
QY 729 LysArgThrAlaGlnLysSerAsnProProLysProLeuLysLysLeuArgPheAspIle 748
DB 2407 AAAAGCAATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2466
QY 749 GlnGlySerAspGlnAlaAspLysSerLysHisLeuProGlyGlnSerLysPheGlnGln 768
DB 2467 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2526
QY 769 LysLeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 788
DB 2527 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2586
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DB 2587 ATGATACCTCAACCAAGGAGAGAAA 2613
RESULT 4
US-09-469-522-50
: Sequence 50, Application US/09469522
: Patent No. US20020151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Henedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESS: Arnold, White & Burke
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER AVAILABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APL: 77210-4433
: FILING DATE: 22-Dec-1999
: CLASSIFICATION: <Unknown>
: PRIORITY INFORMATION:
: APPLICATION NUMBER: 09/026,459
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: PRESTIPULATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: UIX:506
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3554 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..2790
: SEQIDNO: 50
: US-09-469-522-50
Alignment Scores:
Pred. No.: 0 Length: 3554
Score: 4068.50 Matches: 797
Percent Similarity: 85.88% Conservativeness: 0
Best Local Similarity: 85.88% Mismatches: 0
Query Match: 98.18% Indels: 131
DB: 10 Gaps: 1
US-09-026-459a-45 (1-797) x us-09-469-522-50 (1-3554)
QY 1 MetProLeuLysThrProArgLysThrAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 20
DB 7 AlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 56
QY 21 ProAlaProProProProProProProProProProProProProProProProProProPro 40
DB 67 CCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
QY 41 AspLeuProLeuValArgLeuGlnPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 60

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QY 650 ProfileProHisLeuProArgSerProTyrLysPheProSerSerProLeuArgLeuPro 664
DB 2447 CCAATACCCACATCCGCAAGATGCTTAACTTTCTAGTTTAACTTTATGATGATGAT 2406
QY 670 GlycylAsnLeuLysSerProLysSerProLysSerProLysSerProLysSerPro 689
DB 2487 GAGAGAAATATATATATATATATATATATATATATATATATATATATATATATAT 2466
QY 690 ThrProLysMetThrProArgSerArgLeuValSerLeuGlyGlySerPheGly 709
DB 2467 ACACCAACAAAAAGACTCCACATCAACAATCTTACTATCAATTCGCGAATCAATCGG 2526
QY 710 ThrSerGlyPheLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLys 729
DB 2527 ACCTGTCACAACTTCACAAAAAATAATCATCATGATGATTAACACGACGACCTGCTCA 2586
QY 730 ArgSerAlaGlySerAsnProLysProLysProLysProLysProLysProLysPro 749
DB 2587 AGAAGTCTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2646
QY 750 GlySerAspGluAlaAspGlySerLysHisLeuProGlyGlySerLysPheGlyGly 769
DB 2647 GCAATCAATCAACACATCAAGTAAACATCTCCACGACAGACGTCACAAATTCACAGAA 2706
QY 770 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 789
DB 2707 CTGACCAAAATGACTCTCTACTCCAAACGCAATGCAAAAGCAGAAATGAATGATAGCAT 2766
QY 790 AspThrSerAsnLysGluGluLys 797
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RESULT 5

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US-09-469-522-1
: Sequence 1, Application US/09469522
: Patent No. us-6601545A
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED REFIN-BLAST/MA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Burkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #10, Version #130
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/469,522
: FILING DATE: 22-Dec-1999
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/007,454
: FILING DATE: <unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: UTXG:506
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3555 base pairs

```

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: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..2790
: SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-09-469-522-1
Alignment Scores:
Pred. No.: 0 Length: 3555
Score: 4068.50 Matches: 797
Percent Similarity: 85.88% Conservative: 0
Best Local Similarity: 85.88% Mismatches: 0
Query Match: 98.18% Indels: 131
DB: 10 Gaps: 1
US-09-026-459a-45 (1-797) x US-09-469-522-1 (1-3555)
QY 1 MetProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAlaAlaPro 20
DB 7 ATCCGCCCAAAACCCGCCAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 66
QY 21 ProAlaProProProProProProProGluGluAspProGluGluAspSerGlyProGlu 40
DB 67 CCGGACACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 126
QY 41 AspLeuProLeuValArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeu 60
DB 127 GACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
QY 61 CysGlnLysLeuLysLeuProAspHisValArgGluArgAlaTrpLeuThrTrpGluLys 80
DB 187 TGTCCACAAATTAACACATACACATATCTCCACACACACACACACACACACACACAC 246
QY 81 ValSerSerValAspGlyValLeuGlyGlyTyrLeuLysLysLysLysLysLysLys 100
DB 247 GTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306
QY 101 IleCysIlePheIleAlaValAspLeu 110
DB 307 ATCTGCTATCTTTATTGAGAGATTACCTAGATGAGATGCTGCTTAACTTTATTCAGCT 366
QY 110 110
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QY 110 110
DB 427 AGTACCAAGCTTCATAATGCTATGCTCAAGACTGCTTGAAGAGATGCTATGCTTGA 486
QY 110 110
DB 487 CTCTTACGAAATGGAAGAGATGCTGAACTTATATATATATATATATATATATATAT 546
QY 110 110
DB 547 ATATCTACTGAAATTAATCTGCAATTTGGTGGTAAAAAGCTTCTTGGCAATCAATTT 606
QY 110 110
DB 607 GCTAAAGGGAATATATTAATAAAGAAAGATGCTGCTGCTATTTATTTATTTAAAG 666
QY 110 110
DB 667 TGTGCTCTTGAATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 726
QY 111 ---AlaValIleProIleAsnLysSerProArgThrProArgGlyGlnAsnArgSer 129
DB 727 ACACCTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 786
QY 130 AlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGlu 149

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747 GACAGATAGCAAAAATATAGAAAATGATACAAAGATATTGAAGTTCTCTCTAAAGAA 846
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147 CACCAAGCAAAACAAAGAGAGCAAAAAGCTTATTCACAAAATTTTAAATCTTTTAAIG 906
57 AsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArg 189
907 AATTCCTCTGACCTTCTGAAATATCTAAATCTGCAATCTGCAATCTGCAATCTGCAAT 1146
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57 LysThrLeuGluThrAspSerIleAspSerPheGluThrGluArgThrProArgLysSer 229
1027 AAAATCTCTGACCTTCTGAAATATCTAAATCTGCAATCTGCAATCTGCAATCTGCAAT 1086
57 AsnLeuAspGluGluValAsnValIleProProIleThrProValIleThrValMetAsn 249
1087 AATTCCTCTGACCTTCTGAAATATCTAAATCTGCAATCTGCAATCTGCAATCTGCAAT 1146
57 ThrIleThrLeuGluMetIleLeuAsnSerAlaSerAspGluProSerGluAsnLeu 269
1147 AATTCCTCTGACCTTCTGAAATATCTAAATCTGCAATCTGCAATCTGCAATCTGCAAT 1206
57 PheSerTyrPheAsnAspGlyThrValAsnProLysGluSerIleLeuLysArgValLys 289
1207 AATTCCTCTGACCTTCTGAAATATCTAAATCTGCAATCTGCAATCTGCAATCTGCAAT 1266
57 AspIleThrLysGluLysPheAlaLysAlaValGlyGlyGlyCysValGlu 309
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57 ThrGlySerGlnArgTyrIleLysGluValArgLeuTyrTyrArgValMetGluSerMet 329
1327 AATTCCTCTGACCTTCTGAAATATCTAAATCTGCAATCTGCAATCTGCAATCTGCAAT 1386
57 LeuLysSerGluGluGluArgSerIleGlnAsnPheSerLysLeuLeuAsnAspAsn 349
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57 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 369
1447 AATTCCTCTGACCTTCTGAAATATCTAAAGCTCTGCAAGCTCTGCAAGCTCTGCAAG 1506
57 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIleLeuAsnVal 389
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57 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 409
1567 CTTAAATCTGACCTTCTGAAATATCTAAAGCTCTGCAAGCTCTGCAAGCTCTGCAAG 1626
57 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSer 429
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57 LeuAlaIleProLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 449
1687 CTTGATGCTCTGACCTTCTGAAATATCTAAAGCTCTGCAAGCTCTGCAAGCTCTGCAAG 1746
57 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnHis 469
1747 GATCAATCTGACCTTCTGAAATATCTAAAGCTCTGCAAGCTCTGCAAGCTCTGCAAG 1806
57 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysGlySerThrThr 489
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57 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 509
1867 GGTGTAATTTCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAAT 1926

510 ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeu 529
1927 CCATTCAGAAATCTACCT 1986
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610 ArgValLeuIleLysGluGluTyrAspSerIleIleValPheLysAsnSerValPhe 629
2227 GGTCTTTTGTAAAGCT 2286
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2287 ATTCAGACACTGAAACAAATATTTTGTAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2446
650 ProIleProIleIleProArgSerProTyrLysPheProSerProLeuArgIlePro 669
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670 GlyCysAsnIleTyrIleSerProLysSerProTyrLysIleSerGluThrLeuPro 699
2497 GGAGGGAACATCTATTTTGTAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2466
690 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyLysSerPheGly 709
2467 ACACCAACAAATATGATCT 2526
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RESULT 6

US-09-454-531-143
; Sequence 143, Application US/09454531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: weaver, zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09454, 531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/243,143


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470 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysLysThrThr 489
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610 ArgValLeuTyrGlyLeuGluThrTyrAspSerThrLeuValPheLysAsnSerValPhe 629
2358 GCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2417
630 MetGlnArgLeuLysThrAsnLeuLeuGlnTyrAlaSerThrArgProThrLeuSer 649
2418 ATGACAGACACGAAAAAATAATTTGACATGCTTCCACAGCGCGCTTCTTCTTCTTCA 2477
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730 ArgSerAlaGluGlySerAsnProTyrLysLeuLysLysLysLeuArgPheAspThrGlu 749
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2898 CATATGATCAAAACAGGAGACAAA 2921

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RESULT 7

US-09-026-459a-45

: Sequence 7, Application US/09/060211

: Patent No. US2002013712A1

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GENERAL INFORMATION:
APPLICANT: Gregory, Richard J.
Inventor: Willis, Ken N.
Manaval, Daniel C.
TITLE OF INVENTION: Recombinant Adenoviral Vector and
Methods of Use
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crow LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,211
FILING DATE: 18 May 2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,674
FILING DATE: 15 FEB-2000
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25-OCT-1994
APPLICATION NUMBER: US 08/233,669
FILING DATE: 26 APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy S.
REGISTRATION NUMBER: 35,467
REFERENCE/DOCKET NUMBER: 016940-00092005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID No: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2995 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 139..2925
OTHER INFORMATION: /product= "RR"
/Note= "retinoblastoma tumor suppressor"
SEQUENCE DESCRIPTION: SEQ ID No: 7:
US-09-026-459A-45 (1-797) x US-09-026-211-7 (1-2995)

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Alignment Scores:
Pred. No.: 0 Length: 2995
Score: 4058.50 Matches: 796
Percent Similarity: 85.78% Conservative: 0
Best Local Similarity: 85.78% Mismatches: 1
Query Match: 97.94% Indels: 131
DB: 10 Gaps: 1

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QY 1 MetProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaLeuPro 20
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QY 21 ProAlaProProProProProProProProProProProProProProProPro 40
Db 199 CCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 258
QY 41 AspLeuProLeuValArgLeuGluPheGluThrGluGluProAspThrAlaLeu 60
Db 259 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418

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QY	201	AspAlaArgLysPheLeuAspHisAspLysThrLeuGlnThrAspSerLleAspSerPhe	220
IQ	907	CAICCAACAATATTTTTCATCATGATAAAACCTTTCAGACTGATCATATACACAGTTTT	966
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IQ	967	GAACAACAGCAACACACACAAAAAGTAACCTTCATGAGAGGTCGAACTGAATTCCTCCA	1026
QY	241	HisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetLleLeuAsnSer	260
IQ	1027	CAACTCCAGTTAGAGCTGTTTAGAACACTATCCACCAATTAATGATGATTTTANATCCA	1086
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IQ	1087	GTAAGTCATCAACCCTCACAAAICTGATTCCTATTTTAAACAACTCACAGTCGAATCCA	1146
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IQ	1267	TCTATATGAGGTAATGCAATCCATGCTTAATTAATCAGAAAGCAAGCATTTATCCATTCAA	1326
QY	341	AsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu	360
IQ	1327	AAITTAGCAAACTCTCAACACCAACAAATTTTCATATGCTTTATGGCGTGGCTCTT	1386
QY	361	GluValValMetAlaThrTyrSerArgSerThrSerGluAsnLeuAspSerGlyThrAsp	380
IQ	1387	GAGTGTGTAATGAGCAATATATAGCAACATCAATATCAAAATCTATCTTGGCAACAGAT	1446
QY	381	LeuSerPheProIlePheLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal	400
IQ	1447	TCTCTTTCCTCAAGCATCTGAACTGCTTAATTTAAAGCGCTTTGATTTTACAAAGTG	1506
QY	401	IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetLleLysHisLeuGlu	420
IQ	1507	ATCGAAGTITATCAAACTACCAAGCGCACTTCACACACAAAATCAATAAACATTTAGAA	1566
QY	421	ArgCysGluHisArgIleMetGluSerLeuAlaIlePheSerAspSerProLeuPheAsp	440
IQ	1567	CGATGTCAACATCGAATATCAATCTCTTATGCTTATGCTTATGATTCAATTTATTTCAT	1626
QY	441	LeuIleLysGlnSerLysAspArgGluGlyProThrAspHisIleGlnSerAlaCysPro	460
IQ	1627	CTTATTAACAAATCAAAACACCAACCAAGACCAACATGATCATCTCAATTCCTGTGCT	1686
QY	461	LeuAsnLeuProLeuAlaAsnAsnIleThrAlaAlaAspMetTyrLeuSerProValArg	480
IQ	1687	CTTAATCTTCTCTCCAGAAATACACACTCCACACATATGATCTTTCTCTCTGTGAAGA	1746
QY	481	SerProLysLysCysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln	500
IQ	1747	TCTGTAAAGAAAAAGCTTCAACTATAGTGCTGTAAATTCATCTAGTCAATATGACACAAA	1806
QY	501	AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyr	520
IQ	1807	GTAACCTACACCTTCTACATCAGAAAGCAATGAAATCTACCTCTCTTCTCTTTAT	1866
QY	521	LysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSer	540
IQ	1867	AAAAACCTGATCGGCTAGCGTATCTCGGGCTAAATACACTTTCGAAAGCGCTTCTGCT	1926

Qy	541	GLuHisProGluLeuGluHisIleIleThrThrLeuPheGluHisThrLeuGluAsnGlu	560
Db	1927	GAGCAGCCAAATATTAAGATATATCACTGAGATTTTITTTTAAACAATCTGCAAAATGAG	1986
Qy	561	TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIle	580
Db	1987	TATGAACCTCAGCAGACAGGCAATTCGACCAAAATATCACTGCTCTCCATGATACGCAATA	2046
Qy	581	CysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu	600
Db	2047	TGCAAAAGCAAAATAIAGAAGCTTAAATTCAAAATCATTGTAAGAAAGATAAAGAAATCTT	2106
Qy	601	ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluGlyTyrAspSer	620
Db	2167	ACTCATGCTCTTTCAGACATTTCAAAAGATTTTTCATTAAGAAAGAAAGATATATCT	2166
Qy	621	IleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGluTyr	640
Db	2167	ATTATACATATGATTAACCTGGCTCTTCATCCACACACACAAACAAATATTTCCACATAT	2226
Qy	641	AlaSerThrArgProProThrLeuSerProIlePheProHisIleProArgSerProTyrLys	660
Db	2227	CTTTCTCAAGAGAGAGAGAAATTTCTTAAGAAATGATCAATGATCAAGAGATTTTAAG	2286
Qy	661	PheProSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSer	680
Db	2287	TTTCTATAGTTTAAATTAAGATATCTCAAGGAAATATATATATCAAGGCTTAAGAT	2346
Qy	681	ProTyrLysIleSerGluIleProThrProThrLysMetThrProArgSerArgIle	700
Db	2347	CCATATATAAATTTCCAGAGGCTCGCCAAACCAACCAAAATACACTCCAAAGATCAAGAACT	2406
Qy	701	LeuValSerIleGlyIleSerPheGlyThrSerGluLysPheGlnLysIleAsnGluMet	720
Db	2407	TTAGTATCAATTGCTCAATCATTCAGCACTTCTGAGAGAGTTCCAGAGAAATAAATCAATG	2466
Qy	721	ValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPheLysPro	740
Db	2467	GTATGTAAATAGCAATAGTGTCTCAAAAAGATGTCAAGAGAAAGTCAAGTCCGCTTAAACCA	2526
Qy	741	IleuLysLysLeuArgPheAspIleGlySerAsnGlnAlaMetGlySerLysHisLeu	760
Db	2527	CTGAAAAAATACGCTTTTGATATTAAGCATTCAGATCAAGCAGATCGAAGTAAACATCTC	2586
Qy	761	ProGlyuLysLysPheGlnIleLysLeuAlaGluMetThrSerThrArgThrArgMet	780
Db	2587	CCAGAGAAATCTTAAATTTTAAATAAATTAAGAAATCAATTTATTCGAAATAGCAATG	2646
Qy	781	GlnLysGlnLysMetAsnAspSerMetAspThrSerAsuLysGluGlyLys	797
Db	2647	CAAAAGCAAAAAATGAATAGATGATGATGAATCTCAAAATCAAAATCAAAATCAAAATCAAA	2697

RESULT 9

```

RES001 9
US-09-469-522-28
: Sequence 28, Application US/09469522
: Patent No. US202020151461A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Xu, Hong-Ji
:           Hu, Shi-Xue
:           Benedict, William
:           Zhou, Yunli
:
: TITLE OF INVENTION: MEMPHIS
:                   PROTEINS
:
: NUMBER OF SEQUENCES: 51
:
: CORRESPONDENCE ADDRESS:
: ADDRESS: Arnold, White
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
:
: ZIP: 77210-4433
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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QY 444 GluSerLeuAspArgGlnLysProThrAspHisLeuGluSerAlaCysProLeuAsnLeu 463
DB 1630 CAALCAAAACACCAACACACACACACACACACACACACACACACACACACACACAC 1689
QY 464 ProLeuGluAsnAsnHisThrAlaAlaAspMetLysLeuSerProValArgSerProLys 483
DB 1690 CCCTCTGCAAAATAATACACATGACACATATATATATATATATATATATATATATAT 1749
QY 484 LysLysLysSerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSer 503
DB 1750 AAAAAAGGTTCAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1809
QY 504 AlaPheLeuThrGlnLysProLeuLysSerThrSerLeuSerLeuPheLysLysVal 523
DB 1810 GGCCTTCAGACACACAGACACACACACACACACACACACACACACACACACACACAC 1869
QY 524 TyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPro 543
DB 1870 TATGAGTATATATATATATATATATATATATATATATATATATATATATATATAT 1929
QY 544 GluLeuGluHisLeuLeuThrLeuPheGlnHisThrLeuGlnAsnGluLysTyrGluLeu 563
DB 1940 GAAATTAACATATATATATATATATATATATATATATATATATATATATATATAT 1989
QY 564 MetAspAsnArgHisLeuAspHisLeuMetLysSerSerMetLysLysVal 583
DB 1990 ATGACACACAGGACATGACACACACACACACACACACACACACACACACACACAC 2049
QY 584 LysAsnHisLeuLysLeuLysLysLeuValThrAlaTyrLysAspLeuProHisAla 603
DB 2050 AAAAAATAATATATATATATATATATATATATATATATATATATATATATATAT 2109
QY 604 ValGluGlnThrPheLysArgValLeuLeuLysGluGluGluTyrAspSerLeuVal 623
DB 2110 GTTCAGACACATCAAAAGTGTGTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2169
QY 624 PheTyrAsnSerValPheMetGlnArgLeuLysThrAsnHisLeuGlnTyrAlaSerThr 643
DB 2170 TTATATAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2229
QY 644 ArgProProThrLeuSerProLeuProHisLeuProArgSerProTyrLysPheProSer 663
DB 2240 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2289
QY 664 SerProLeuArgLysProGlyAsnLysLysLysLysLysLysLysLysLysLysLys 683
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QY 684 IleSerGluLysLeuProThrProThrLysMetThrProArgSerArgIleLeuValSer 703
DB 2350 ATTTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2409
QY 704 IleLysLysSerPheLysThrSerGlnLysPheGlnLysIleAsnHisLeuValLysAsn 723
DB 2410 ATTATGATATATATATATATATATATATATATATATATATATATATATATATATAT 2469
QY 724 SerAspArgValLeuLysArgSerAlaGluCysSerAspProPheLysProLeuLysLys 743
DB 2470 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2529
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QY 764 SerLysPheGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGln 783
DB 2590 TCCAAATTCACACAAAATGGAACAAATATATATATATATATATATATATATATATATAT 2649
QY 784 LysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 797
DB 2650 AAAATGAATGATAGCATGATATATATATATATATATATATATATATATATATATATAT 2691

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RESULT 10
US-09-469-522-48
: Sequence 48, Application US/09469522
: Patent No. US20020151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED REINOLASIOMA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1 0, Version #1 30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09-469-522
: FILING DATE: 22-DEC-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/026,459
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: UTXC:506
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3383 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..2619
: SEQUENCE DESCRIPTION: SEQ ID NO: 48.
US-09-469-522-48

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Alignment Scores:
Prod. No.: 0 Length: 3383
Score: 3799.00 Matches: 755
Percent Similarity: 87.21% Conservative: 9
Best Local Similarity: 96.10% Mismatches: 28
Query Match: 91.67% Indels: 84
DB: 10 Gaps: 6

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US-09-026-459a-45 (1-797) x US-09-469-522-48 (1-3383)
QY 1 MelProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAlaGluPro 20
DB 7 ATGCGGCTAAACCGCGGAAAAACGGCGGCGCAACCGCGCGCGCGCGCGCGCGCAACCC 64
QY 21 ProAlaProProProProProProProProProProProProProProProProPro 40
DB 67 CAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126
QY 41 AspLeuProLeuValArgLeuGluPheGluGluThrGluGluProAspPheLeuAlaLeu 60
DB 127 GACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186
QY 61 CysGlnLysLeuLysIleProAspHisValArgGluArgAlaTrpLeuThrTrpGluLys 80

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ADDRESSEE: Arnold, White & Burke
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522

FILING DATE: 22-Dec-1999

CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: Hubert, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: OTX:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418,8000

TELEFAX: 512/474,7477

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 4113 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: Linear

FEATURES:

NAME/KEY: CDS

LOCATION: 7..2449

SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US 09 469 522 46

Alignment Scores:

Prod. No.: 0 Length: 4113
Score: 4500.000 Matches: 607
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.67% Indels: 0
Gaps: 0

US 09 026 459a 45 (1 797) x US 09 469 522 46 (1 4113)

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27 141 AratleAlaLysGlnLeuGluAsnAspThrAratlelleGluValLeuGlyLysGlnHis 150
146 449 GAGATACAAAATTAATACAAAATGTTATTTGAAAATTTTATATCTTTTATATGAAT 468
27 151 GluYSAsnThrAspGlnValLysAsnValTyrPheLysAsnThrLeuPheMetAsn 170
146 409 CAATGTAATATATATGAG 468
27 171 SerLeuGlyLeuValThrSerAsnGlyLeuProGlnValGluAsnLeuSerLysArgTyr 190
146 469 ATCTTTCAGCTTCTGAAATACGACATTCAGACATTCAGACATTCAGACATTCAGACATTC 528
27 191 GluGlnIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
146 529 CAATGTAATATATATGAG 588
27 211 ThrLeuGlnThrAspSerThrAspSerPheGlnThrGluArgThrProArgLysSerAsn 230
146 589 ACTCTTCAGCTTCTGAG 648
27 241 LeuAspGlnValAlaAsnValThrProHisThrProValArgThrValMetAsnThr 250

Db 649 CTTCATCAACAGAGGTAAAGTAAATCTCTCCACACACATCTCCATAGATACGTAAGAAAT 708
QY 251 IleGlnGlnLeuMetIleLeuAsnSerAlaSerAspGlnProSerGlnAsnLeuIle 270
Db 709 ATCCACAAATTAATGATGATTTTAAATTCAGTAAGGATGATCAAGCTTTCAGAAAATCTGAT 768
QY 271 SerTyrPheAsnAspCysThrValAsnProLysGlnSerIleLeuLysArgValLysAsp 290
Db 769 TCCATTTTAAACAATCGACAGTGAATCCAAAAGAAATATATCTGAAAAGAGATGAAGAT 828
QY 291 IleGlyTyrIlePheLysGlnLysPheAlaLysAlaValLysGlnGlyLysValGlnIle 310
Db 829 ATAGTATACATCTTAAAGCAAAATTCGCTAAAGCTCTGCGACATAGGCTTCTGCTGAAAAT 888
QY 311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlnGlnSerMetLeu 330
Db 889 GGAATCAAGAGATAAANAGAGATTCGCTAAAGCTCTGCGACATAGGCTTCTGCTGAAAAT 948
QY 331 LysSerGlnGlnIleArgLeuSerIleGlnAsnPheSerLysGlnGlnAspAsnIle 950
Db 949 AAATCAAGAGAGAGAGATTCATGCTTCAAAAATTTTAGCAAAATTCGTAATGAAATTT 1008
QY 351 PheHisMetSerLeuLeuAlaCysAlaLeuGlnValValMetAlaIleThrTyrSerArgSer 370
Db 1009 TTTCAATATGCTTTTATTCGGTCTGCTCTCTGAGCTTCTGAGGCTCAATAGAGAGAGAGAG 1068
QY 371 ThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProThrIleLeuAsnValLeu 390
Db 1069 ACATCTCAGAAATCTGATTCGGAATAGATTCGCTCTTAAATTCGCTGAGATTCGATTCGCT 1128
QY 391 AsnLeuLysAlaPheAspPheTyrLysValIleGlnSerPheIleLysGlnSerLysAspAla 410
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Db 1309 GCAATCTGATCAGCTTGAATCTGCTTCTGCTTAAATTCGCTGCTGCTGCTGCTGCTGCTG 1368
QY 471 AlaAlaAspMetTyrLeuSerProValArgSerProLysGlnSerLysGlnSerThrThrArg 490
Db 1369 GCAATCAATATGATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1428
QY 491 ValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
Db 1429 GTAAATCTCTACGCAATGAG 1488
QY 511 LeuLysSerThrSerLeuSerLeuPheTyrLysValTyrArgLeuAlaValLeuArg 530
Db 1489 TTGAAATCT 1548
QY 531 LeuAsnThrLeuGlyGlnArgLeuLeuSerGlnHisProGlnLeuGlnHisIleThrIleTyr 550
Db 1549 CTAATAACATCTCTGAAACGCT 1608
QY 551 ThrLeuPheGlnHisThrLeuGlnAsnGlnTyrGlnLeuMetArgAspArgHisLeuAsp 570
Db 1609 AGCTTTTTCAGCAACACCTCTGAGAAATGAGATAGAAATGAGAGAGAGAGAGAGAGAGAGAG 1668
QY 571 GlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLysPhe 590
Db 1669 CAATTTATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1728
QY 591 LysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGlnThrPheLysArg 610
Db 1729 AAAATCATCTTAACAGCAATACAGGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1788


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1054 AAAATCAAGCAAGCAATTAATCAATCAAAAATTAAGCAAACTTCGAAAGCAACAT 1113
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1114 TTTCAATAGTCTTATATGGTGGTGGCTCTGAGCTGTAAATGGACACATATACAGAAG 1173
QY ThrSerGlnAsnGluAspSerGlyThrAspLeuSerPheProIleIleLeuAsnValLeu 390
1174 AATCTAGAAATCTGATCTGGAAACAGATTTGCTTTCCATGGATCTGAATGTGCT 1233
QY AsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
1234 AAATTAAGAGTTCATATTTTAAAGAGCAAGCAAACTTTATCAAAAGCAGAAAGCAAC 1293
QY LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeu 430
1294 TTTCAACACAGAAACATCAAAAATTTTACAGCAAGCAAGCAATCAAAATCAAGATCCCT 1353
QY AlaIleProLeuSerAspSerProLeuPheAspGluIleLysGlnSerLysAspArgGluGly 450
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QY LeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGlnLeuGluHisIleIleTrp 550
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QY ThrLeuPheGlnHisThrLeuGluAsnGluTyrGlnLeuMetArgAspArgHisLeuAsp 570
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1894 GTTTGATCAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1953
QY GlnArgLeuLysThrAsnIleLeuIleTyrAlaSerThrArgProProThrLeuSerPro 650
1954 CAGACATCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2013
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2014 ATAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2073
QY GlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProThr 690
2074 GAGAAATCTATATTTTCAATCTGATGATGATGATGATGATGATGATGATGATGATGATG 2133
QY ProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710

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DB 2134 CCAATCAAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2193
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DB 2194 TCTGAGAAAGTTCCAGAAAATAATATCAATGATGATGATGATGATGATGATGATGATGAT 2253
QY 731 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluGly 750
DB 2254 AGTGTGAAGGAAGCAACCTCTTAACCTGAAAAAACTGAAAAAACTGAAAAAACTG 2313
QY 751 SerAspGluAlaAspGlySerLysHisLeuProLysGlnSerLysPheGlnGluLysLeu 770
DB 2314 TCAGATCAAGCAGATGCAAGTAAACATCTCTCAAGCAGATCTCTCAAGCAGATCTCT 2373
QY 771 AlaGluMetThrSerThrArgThrArgMetGluGlySerLysMetAsnAspSerMetAsp 790
DB 2474 GCATCAAAATGATCTCTCTCTCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2533
QY 791 ThrSerAsnLysGluGluLys 797
DB 2434 AGCTCAAAATCAAGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2493

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Search completed: January 19, 2003, 05:44:48
Job time : 139.18 secs

